GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:57:15 ; Search time 64.5571 Seconds
(without alignments)
3937.467 Million cell updates/sec

Title: US-10-683-775-1_COPY_80_222
Perfect score: 143
Sequence: 1 aatttgtgatgctattgctt.....aaaacctctacaaatgtggt 143

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	143	100.0	222	3	US-09-687-050-1	Sequence 1, Appli
c	2	143	100.0	222	3	US-09-687-050-3	Sequence 3, Appli
c	3	131	91.6	230	3	US-09-448-256-1	Sequence 1, Appli
c	4	131	91.6	230	3	US-09-928-463A-1	Sequence 1, Appli
	5	131	91.6	296	3	US-09-068-880-2	Sequence 2, Appli
	6	131	91.6	677	2	US-08-644-664B-3	Sequence 3, Appli
	7	131	91.6	677	2	US-08-761-277A-3	Sequence 3, Appli
c	8	131	91.6	717	3	US-09-496-445-3	Sequence 3, Appli
c	9	131	91.6	782	3	US-09-714-550-8	Sequence 8, Appli
c	10	131	91.6	1078	3	US-09-310-842-1	Sequence 1, Appli
c	11	131	91.6	1318	3	US-09-310-842-3	Sequence 3, Appli
c	12	131	91.6	1417	3	US-09-310-842-5	Sequence 5, Appli
c	13	131	91.6	1645	3	US-09-310-842-2	Sequence 2, Appli
c	14	131	91.6	1870	3	US-09-310-842-4	Sequence 4, Appli
c	15	131	91.6	2792	3	US-08-994-689C-8	Sequence 8, Appli
c	16	131	91.6	3218	3	US-09-496-445-4	Sequence 4, Appli
c	17	131	91.6	3282	2	US-08-276-852-154	Sequence 154, App
	18	131	91.6	3282	2	US-08-276-852-169	Sequence 169, App
c	19	131	91.6	3282	2	US-08-899-575-154	Sequence 154, App
	20	131	91.6	3282	2	US-08-899-575-169	Sequence 169, App
c	21	131	91.6	3282	2	US-08-899-575-154	Sequence 154, App
	22	131	91.6	3282	2	US-08-899-575-169	Sequence 169, App
c	23	131	91.6	3282	6	PCT-US95-08743-154	Sequence 154, App
	24	131	91.6	3282	6	PCT-US95-08743-169	Sequence 169, App
c	25	131	91.6	3318	3	US-08-169-613A-1	Sequence 1, Appli
	26	131	91.6	3327	3	US-09-628-730-56	Sequence 56, Appl
	27	131	91.6	3369	3	US-09-628-730-48	Sequence 48, Appl
	28	131	91.6	3705	3	US-09-282-996-3	Sequence 3, Appli
	29	131	91.6	3740	3	US-08-955-565A-6	Sequence 6, Appli
c	30	131	91.6	3822	3	US-08-675-566-8	Sequence 8, Appli
c	31	131	91.6	3944	2	US-07-678-408A-1	Sequence 1, Appli
	32	131	91.6	3954	3	US-09-628-730-53	Sequence 53, Appl
	33	131	91.6	3954	3	US-09-628-730-57	Sequence 57, Appl
c	34	131	91.6	3955	3	US-08-675-566-10	Sequence 10, Appl
	35	131	91.6	3976	3	US-09-628-730-49	Sequence 49, Appl
c	36	131	91.6	4009	3	US-08-675-566-9	Sequence 9, Appli
	37	131	91.6	4059	2	US-08-564-313-2	Sequence 2, Appli
	38	131	91.6	4059	6	PCT-US94-06069-2	Sequence 2, Appli
c	39	131	91.6	4069	3	US-09-170-496D-287	Sequence 287, App
	40	131	91.6	4069	3	US-09-170-496D-288	Sequence 288, App
c	41	131	91.6	4069	3	US-09-364-425B-52	Sequence 52, Appl
	42	131	91.6	4069	3	US-09-364-425B-53	Sequence 53, Appl
c	43	131	91.6	4273	3	US-08-795-430-3	Sequence 3, Appli
c	44	131	91.6	4273	3	US-09-355-700-3	Sequence 3, Appli
c	45	131	91.6	4273	3	US-08-601-132-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-687-050-1
; Sequence 1, Application US/09687050
; Patent No. 6632637
; GENERAL INFORMATION:
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: VECTORS AND METHODS FOR RECOMBINANT PROTEIN EXPRESSION
; FILE REFERENCE: 2902-A
; CURRENT APPLICATION NUMBER: US/09/687,050
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,177
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 222
; TYPE: DNA
; ORGANISM: SV40
US-09-687-050-1

Query Match 100.0%; Score 143; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.8e-32;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 199

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
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Db        200 AGTAAAACCTCTACAAATGTGGT 222
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RESULT 2
US-09-687-050-3/c
; Sequence 3, Application US/09687050
; Patent No. 6632637
; GENERAL INFORMATION:
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: VECTORS AND METHODS FOR RECOMBINANT PROTEIN EXPRESSION
; FILE REFERENCE: 2902-A
; CURRENT APPLICATION NUMBER: US/09/687,050
; CURRENT FILING DATE: 2000-10-12

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;  PRIOR APPLICATION NUMBER:  60/159,177
;  PRIOR FILING DATE:  1999-10-13
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 222
;   TYPE: DNA
;   ORGANISM: SV40
US-09-687-050-3

  Query Match            100.0%;  Score 143;  DB 3;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-32;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        143 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 84

Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 24

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||
Db         23 AGTAAAACCTCTACAAATGTGGT 1


RESULT 3
US-09-448-256-1/c
; Sequence 1, Application US/09448256
; Patent No. 6326193
; GENERAL INFORMATION:
;  APPLICANT: Liu, Leo
;  TITLE OF INVENTION: Insect Control Agent
;  FILE REFERENCE: 2002630-0002
;  CURRENT APPLICATION NUMBER: US/09/448,256
;  CURRENT FILING DATE:  1999-11-24
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 230
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:SV 40
;   OTHER INFORMATION: Transcriptional Terminator Sequence
US-09-448-256-1

  Query Match            91.6%;  Score 131;  DB 3;  Length 230;
  Best Local Similarity  98.6%;  Pred. No. 8.4e-29;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        162 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 103

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 43

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         42 CAAGTAAAACCTCTACAAATGTGGT 18


RESULT 4
US-09-928-463A-1/c
; Sequence 1, Application US/09928463A
; Patent No. 6846482
; GENERAL INFORMATION:
;  APPLICANT: Liu, Leo
;  APPLICANT:  Chouinard, Scott
;  APPLICANT:  Velema, James
;  TITLE OF INVENTION: Insect Control Agent
;  FILE REFERENCE: 2002630-0011
;  CURRENT APPLICATION NUMBER: US/09/928,463A
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 230
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:SV 40
;   OTHER INFORMATION: Transcriptional Terminator Sequence
US-09-928-463A-1

  Query Match            91.6%;  Score 131;  DB 3;  Length 230;
  Best Local Similarity  98.6%;  Pred. No. 8.4e-29;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db        162 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 103

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db        102 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 43

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db         42 CAAGTAAAACCTCTACAAATGTGGT 18


RESULT 5
US-09-068-880-2
; Sequence 2, Application US/09068880B
; Patent No. 6203982
; GENERAL INFORMATION:
;  APPLICANT: Nunokawa, Youichi
;  APPLICANT: Oikawa, Shinzo
;  APPLICANT: Tanaka, Shoji
;  TITLE OF INVENTION: Method for Screening Compounds
;  TITLE OF INVENTION: Regulating the Expression of Human-Inducible Nitric Oxide
;  TITLE OF INVENTION: Synthase
;  FILE REFERENCE: SHIM-001
;  CURRENT APPLICATION NUMBER: US/09/068,880B
;  CURRENT FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: PCT/JP97/03303
;  EARLIER FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 296
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SV40-derived poly A addition region
US-09-068-880-2

  Query Match            91.6%;  Score 131;  DB 3;  Length 296;
  Best Local Similarity  98.6%;  Pred. No. 9e-29;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Db        106 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 165

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        226 CAAGTAAAACCTCTACAAATGTGGT 250
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RESULT 6
US-08-644-664B-3
; Sequence 3, Application US/08644664B
; Patent No. 5776746
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Gene Amplication Methods
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/644,664B
;      FILING DATE:  01-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  GENITOPE-00912
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  677 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-644-664B-3

  Query Match             91.6%;  Score 131;  DB 2;  Length 677;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        202 CAAGTAAAACCTCTACAAATGTGGT 226


RESULT 7
US-08-761-277A-3
; Sequence 3, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  677 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-761-277A-3

  Query Match             91.6%;  Score 131;  DB 2;  Length 677;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db         82 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 141

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 201

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        202 CAAGTAAAACCTCTACAAATGTGGT 226


RESULT 8
US-09-496-445-3/c
; Sequence 3, Application US/09496445
; Patent No. 6693226
; GENERAL INFORMATION:
;  APPLICANT: McNeish, John D.
;  APPLICANT: Ahlijnian, Michael K
;  TITLE OF INVENTION: Transgenic Animals Expressing Human p25
;  FILE REFERENCE: PC10142A
;  CURRENT APPLICATION NUMBER: US/09/496,445
;  CURRENT FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Rous sarcoma virus
US-09-496-445-3

  Query Match             91.6%;  Score 131;  DB 3;  Length 717;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Qy          59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db         576 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 517

Qy         119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db         516 CAAGTAAAACCTCTACAAATGTGGT 492


RESULT 9
US-09-714-550-8/c
; Sequence 8, Application US/09714550
; Patent No. 6558948
; GENERAL INFORMATION:
;  APPLICANT: Kochanek, Stefan
;  APPLICANT:  Schiedner, Gudrun
;  TITLE OF INVENTION: Permanent amniocytic cell line, its
;  TITLE OF INVENTION:  production and use for the production of gene transfer
;  TITLE OF INVENTION:  vectors
;  FILE REFERENCE: 50125/007002
;  CURRENT APPLICATION NUMBER: US/09/714,550
;  CURRENT FILING DATE:  2000-11-16
;  PRIOR APPLICATION NUMBER: US 60/167,439
;  PRIOR FILING DATE: 1999-11-23
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-09-714-550-8

  Query Match             91.6%;  Score 131;  DB 3;  Length 782;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy           1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Qy          59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db         636 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 577

Qy         119 CAAGTAAAACCTCTACAAATGTGGT 143
               |||||||||||||||||||||||||
Db         576 CAAGTAAAACCTCTACAAATGTGGT 552


RESULT 10
US-09-310-842-1/c
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1078
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1078)
;   OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2 can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1077)..(1078)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
;   OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-1

  Query Match             91.6%;  Score 131;  DB 3;  Length 1078;
  Best Local Similarity   98.6%;  Pred. No. 1.2e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy           1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db         990 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 931

Qy          59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         930 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 871

Qy         119 CAAGTAAAACCTCTACAAATGTGGT 143
               |||||||||||||||||||||||||
Db         870 CAAGTAAAACCTCTACAAATGTGGT 846


RESULT 11
US-09-310-842-3/c
; Sequence 3, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1318
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1318)
;   OTHER INFORMATION: GM-CSF; Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
;   OTHER INFORMATION: position 1 to 2  can be modified with amino or carboxy
;   OTHER INFORMATION: features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1317)..(1318)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1317
;   OTHER INFORMATION: to 1318  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
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US-09-310-842-3

Query Match 91.6%; Score 131; DB 3; Length 1318;
Best Local Similarity 98.6%; Pred. No. 1.3e-28;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1230 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 1171

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 1111

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db       1110 CAAGTAAAACCTCTACAAATGTGGT 1086
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RESULT 12
US-09-310-842-5/c
; Sequence 5, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1417)
; OTHER INFORMATION: Interleukin-7 (IL-7); Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1416)..(1417)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1416
; OTHER INFORMATION: to 1417 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-5

Query Match 91.6%; Score 131; DB 3; Length 1417;
Best Local Similarity 98.6%; Pred. No. 1.3e-28;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1329 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 1270

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 1210

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db       1209 CAAGTAAAACCTCTACAAATGTGGT 1185
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RESULT 13
US-09-310-842-2/c
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1645)
; OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
; OTHER INFORMATION: Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
; OTHER INFORMATION: position 1 to 2 can be modified with amino or caroxy
; OTHER INFORMATION: features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1644)..(1645)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
; OTHER INFORMATION: to 1645 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-2

Query Match 91.6%; Score 131; DB 3; Length 1645;
Best Local Similarity 98.6%; Pred. No. 1.4e-28;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1557 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 1498

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1497 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 1438

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db       1437 CAAGTAAAACCTCTACAAATGTGGT 1413
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RESULT 14
US-09-310-842-4/c
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4

```
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

  Query Match             91.6%;  Score 131;  DB 3;  Length 1870;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1782 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 1723

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1722 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 1663

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db       1662 CAAGTAAAACCTCTACAAATGTGGT 1638


RESULT 15
US-08-994-689C-8/c
; Sequence 8, Application US/08994689C
; Patent No. 6613958
;  GENERAL INFORMATION:
;    APPLICANT:  Neuhold, Lisa
;    APPLICANT:  Killar, Loran
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL MODEL FOR
;    TITLE OF INVENTION:  DEGENERATIVE DISEASES OF CARTILAGE
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/994,689C
;      FILING DATE:  1997-12-19
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Reza
;      REGISTRATION NUMBER:  38,475
;      REFERENCE/DOCKET NUMBER:  0630/0D532
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2792 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-994-689C-8

  Query Match             91.6%;  Score 131;  DB 3;  Length 2792;
  Best Local Similarity   98.6%;  Pred. No. 1.6e-28;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       2679 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 2620

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 2560

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db       2559 CAAGTAAAACCTCTACAAATGTGGT 2535


Search completed: November 22, 2005, 01:25:58
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:49:09 ; Search time 1903.45 Seconds
(without alignments)
6629.665 Million cell updates/sec

Title: US-10-683-775-3
Perfect score: 222
Sequence: 1 accacatttgtagaggtttt.....gtatcttatcatgtctggat 222

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
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4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pr:*
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10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	222	100.0	222	6	AR408763	AR408763 Sequence
	2	222	100.0	222	6	AR408765	AR408765 Sequence
c	3	222	100.0	222	6	AX113060	AX113060 Sequence
	4	222	100.0	222	6	AX113062	AX113062 Sequence
c	5	210	94.6	573	8	HSA332357	AJ332357 Homo sapi
c	6	210	94.6	667	6	AX114869	AX114869 Sequence
c	7	210	94.6	677	6	AR016495	AR016495 Sequence
c	8	210	94.6	677	6	AR096878	AR096878 Sequence
c	9	210	94.6	677	6	BD136073	BD136073 Vaccines
	10	210	94.6	717	6	AR476069	AR476069 Sequence
	11	210	94.6	717	6	BD002329	BD002329 Transgeni
c	12	210	94.6	770	6	AX114868	AX114868 Sequence
	13	210	94.6	782	6	AR310572	AR310572 Sequence
	14	210	94.6	782	6	AX150253	AX150253 Sequence
	15	210	94.6	1096	11	AY590429	AY590429 Cloning v
c	16	210	94.6	1433	6	CQ971831	CQ971831 Sequence
	17	210	94.6	1447	11	AF140802	AF140802 Expressio
	18	210	94.6	1513	11	AF140800	AF140800 Expressio
	19	210	94.6	1513	11	AF140801	AF140801 Expressio
c	20	210	94.6	1578	6	CS038903	CS038903 Sequence
	21	210	94.6	1723	11	SYNIL2S	L78438 Synthetic S
	22	210	94.6	2143	11	SYNDSP2	K03394 Synthetic p
c	23	210	94.6	2197	6	CQ971825	CQ971825 Sequence
	24	210	94.6	2792	6	BD231755	BD231755 Transgeni
	25	210	94.6	2792	6	AR392743	AR392743 Sequence
c	26	210	94.6	2860	11	PSBC2	X68258 Bicistronic
	27	210	94.6	2932	6	I07209	I07209 Sequence 3
	28	210	94.6	2932	6	BD015183	BD015183 TLiSa cel
c	29	210	94.6	3058	6	A93936	A93936 Sequence 1
c	30	210	94.6	3123	11	PMBC2TD	X77750 Plasmid pMB
c	31	210	94.6	3146	11	CVU89931	U89931 Cloning vec
	32	210	94.6	3160	11	PSVSPORT	U14626 Cloning vec
	33	210	94.6	3218	6	AR476070	AR476070 Sequence
	34	210	94.6	3218	6	BD002330	BD002330 Transgeni
	35	210	94.6	3263	6	E28258	E28258 Purificatio
	36	210	94.6	3263	6	AX002278	AX002278 Sequence
	37	210	94.6	3280	11	UCU89963	U89963 Cloning vec
	38	210	94.6	3318	6	AR257484	AR257484 Sequence
	39	210	94.6	3396	11	ASPSG424	X85976 Plasmid pSG
	40	210	94.6	3485	11	UCU89962	U89962 Cloning vec
c	41	210	94.6	3487	11	PSBC1	X68257 Bicistronic
c	42	210	94.6	3639	11	SYNPKA1	D13749 Unidentifie
c	43	210	94.6	3740	6	AR262814	AR262814 Sequence
c	44	210	94.6	3807	11	CVU51223	U51223 Cloning vec
	45	210	94.6	3900	6	I07249	I07249 Sequence 9

ALIGNMENTS

RESULT 1
AR408763/c
LOCUS AR408763 222 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6632637.
ACCESSION AR408763
VERSION AR408763.1 GI:40159158
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 222)
AUTHORS McGrew,J.T.
TITLE Vectors and methods for recombinant protein expression
JOURNAL Patent: US 6632637-A 1 14-OCT-2003;
Immunex Corporation; Seattle, WA
FEATURES Location/Qualifiers
source 1. .222
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 222; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 8.2e-36;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 163

Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 103

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 43

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db         42 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1
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RESULT 2
AR408765
LOCUS       AR408765                222 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 3 from patent US 6632637.
ACCESSION   AR408765
VERSION     AR408765.1  GI:40159160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 222)
  AUTHORS   McGrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: US 6632637-A 3 14-OCT-2003;
            Immunex Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 222;  DB 6;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-36;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60

Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222


RESULT 3
AX113060/c
LOCUS       AX113060                222 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 1 from Patent WO0127299.
ACCESSION   AX113060
VERSION     AX113060.1  GI:13939494
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Mcgrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: WO 0127299-A 1 19-APR-2001;
            Immunex CorporatioN (US)
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="Simian virus 40"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
ORIGIN

  Query Match           100.0%;  Score 222;  DB 6;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-36;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 163

Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 103

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 43

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         42 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1


RESULT 4
AX113062
LOCUS       AX113062                222 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 3 from Patent WO0127299.
ACCESSION   AX113062
VERSION     AX113062.1  GI:13939496
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Mcgrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: WO 0127299-A 3 19-APR-2001;
            Immunex CorporatioN (US)
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="Simian virus 40"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
ORIGIN

  Query Match           100.0%;  Score 222;  DB 6;  Length 222;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-36;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60

Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222


RESULT 5
HSA332357/c
LOCUS       HSA332357               573 bp    DNA     linear   PRI 18-JUL-2002
DEFINITION  Homo sapiens genomic sequence surrounding NotI site, clone
            HSJ4P-P16RS.
ACCESSION   AJ332357
VERSION     AJ332357.1  GI:15876775
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
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            Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
  TITLE     NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
  JOURNAL   Nucleic Acids Res. 30 (14), 3163-3170 (2002)
   PUBMED   12136098
REFERENCE   2  (bases 1 to 573)
  AUTHORS   Zabarovsky,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="HSJ4P-P16RS"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 8;  Length 573;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 191

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        190 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 131

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 71

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         70 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 27


RESULT 6
AX114869/c
LOCUS       AX114869                667 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 29 from Patent WO0129208.
ACCESSION   AX114869
VERSION     AX114869.1  GI:14031811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 29 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA sequence derived from vector pRK80c"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 667;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 493

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        492 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 433

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 373

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        372 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 329


RESULT 7
AR016495/c
LOCUS       AR016495                677 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5776746.
ACCESSION   AR016495
VERSION     AR016495.1  GI:3972772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Denney,D.W. Jr.
  TITLE     Gene amplification methods
  JOURNAL   Patent: US 5776746-A 3 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 167

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        166 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 107

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 47

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         46 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3


RESULT 8
AR096878/c
LOCUS       AR096878                677 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 3 from patent US 5972334.
ACCESSION   AR096878
VERSION     AR096878.1  GI:10009402
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Denney,D.W. Jr.
  TITLE     Vaccines for treatment of lymphoma and leukemia
  JOURNAL   Patent: US 5972334-A 3 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 677;
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  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 167

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        166 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 107

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 47

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         46 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3


RESULT 9
BD136073/c
LOCUS       BD136073                677 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vaccines for treatment of lymphoma and leukemia.
ACCESSION   BD136073
VERSION     BD136073.1  GI:23231018
KEYWORDS    JP 2002509426-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Jr,D.W.D.
  TITLE     Vaccines for treatment of lymphoma and leukemia
  JOURNAL   Patent: JP 2002509426-A 3 26-MAR-2002;
            GENITOPE CORP
COMMENT     OS   Unidentified
            PN   JP 2002509426-A/3
            PD   26-MAR-2002
            PF   25-APR-1997 JP 1997539097
            PR   01-MAY-1996 US    08/644664,06-DEC-1996 US    08/761277 PI
            DAN W DENNEY JR
            PC   C12N15/86,C12N15/63,C12N15/00,C12P19/24,A61K39/395,C07H21/04
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   Vaccines for treatment of lymphoma and leukemia FH   Key
             Location/Qualifiers
            FT   source          1. .677
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .677
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 167

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        166 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 107

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 47

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         46 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3


RESULT 10
AR476069
LOCUS       AR476069                717 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 3 from patent US 6693226.
ACCESSION   AR476069
VERSION     AR476069.1  GI:42716014
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   McNeish,J.D. and Ahlijanian,M.K.
  TITLE     Transgenic mice expressing human p25
  JOURNAL   Patent: US 6693226-A 3 17-FEB-2004;
            Pfizer Inc; New York, NY
FEATURES              Location/Qualifiers
     source           1. .717
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 717;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 551

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        552 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 611

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 671

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        672 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 715


RESULT 11
BD002329
LOCUS       BD002329                717 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Transgenic non-human animal having transgene encoding p25
            polypeptide and  transgenic non-human mammalian cell.
ACCESSION   BD002329
VERSION     BD002329.1  GI:18630290
KEYWORDS    JP 2000224995-A/3.
SOURCE      Rous sarcoma virus
  ORGANISM  Rous sarcoma virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Alpharetrovirus.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Arijanian,M.K. and Macnesh,J.D.
  TITLE     Transgenic non-human animal having transgene encoding p25
            polypeptide and transgenic non-human mammalian cell
  JOURNAL   Patent: JP 2000224995-A 3 15-AUG-2000;
            PFIZER PROD INC
COMMENT     OS   Rous sarcoma virus
            PN   JP 2000224995-A/3
            PD   15-AUG-2000
            PF   03-FEB-2000 JP 2000026792
            PR   03-FEB-1999 US    60/118478
            PI   MICHAEL KIRK ARIJANIAN,JOHN DOUGLAS MACNESH
            PC   C12N15/09,A01K67/027,A61K45/00,A61P25/28,C12N5/10,C12N9/12, PC
              C12N9/99//
            PC   G01N33/15,G01N33/50,(C12N5/10,C12R1:91),C12N15/00,C12N5/00, PC
              (C12N5/00,C12R1:91)
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            FH   Key             Location/Qualifiers
            FT   source          1. .717
            FT                   /organism='Rous sarcoma virus'.
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="Rous sarcoma virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:11886"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 717;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 551

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        552 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 611

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 671

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        672 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 715


RESULT 12
AX114868/c
LOCUS       AX114868                770 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 28 from Patent WO0129208.
ACCESSION   AX114868
VERSION     AX114868.1  GI:14031810
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 28 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA squence derived from vector pRK80b"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 770;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 599

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        598 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 539

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 479

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        478 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 435


RESULT 13
AR310572
LOCUS       AR310572                782 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8 from patent US 6558948.
ACCESSION   AR310572
VERSION     AR310572.1  GI:31703586
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 782)
  AUTHORS   Kochanek,S. and Schiedner,G.
  TITLE     Permanent amniocytic cell line, its production and use for the
            production of gene transfer vectors
  JOURNAL   Patent: US 6558948-A 8 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 611

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        612 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 671

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 731

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        732 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 775


RESULT 14
AX150253
LOCUS       AX150253                782 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 8 from Patent WO0136615.
ACCESSION   AX150253
VERSION     AX150253.1  GI:14348273
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Kochanek,S. and Schiedner,G.
  TITLE     Permanent amniocyte cell line, the production thereof and its use
            for producing gene transfer vectors
  JOURNAL   Patent: WO 0136615-A 8 25-MAY-2001;
            Kochanek, Stefan (DE)
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="Simian virus 40"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
                     /note="3'-Spleiss- und Polyadenylierungssignal von SV40
                     aus Plasmid pGL2basic, entsprechend bp 1978-2749, Genbank
                     X65323"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-33;
```

```
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 611

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        612 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 671

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 731

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        732 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 775


RESULT 15
AY590429
LOCUS       AY590429               1096 bp    DNA     linear   SYN 05-AUG-2004
DEFINITION  Cloning vector pACCMVpLpARS(+), partial sequence.
ACCESSION   AY590429
VERSION     AY590429.1  GI:46370406
KEYWORDS    .
SOURCE      Cloning vector pACCMVpLpARS(+)
  ORGANISM  Cloning vector pACCMVpLpARS(+)
            other sequences; artificial sequences; vectors.
REFERENCE   1  (bases 1 to 1096)
  AUTHORS   Sapag,A., Munoz-Brauning,C. and Israel,Y.
  TITLE     Hammerhead ribozymes decrease the activity of rat mitochondrial
            aldehyde dehydrogenase (ALDH2)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1096)
  AUTHORS   Munoz-Brauning,C. and Sapag,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2004) Laboratorio de Farmacoterapia Genica,
            Departamento de Quimica Farmacologica y Toxicologica, Facultad de
            Ciencias Quimicas y Farmaceuticas, Universidad de Chile, Olivos
            1007, Independencia, Santiago 8380492, Chile
FEATURES             Location/Qualifiers
     source          1. .1096
                     /organism="Cloning vector pACCMVpLpARS(+)"
                     /mol_type="other DNA"
                     /db_xref="taxon:271169"
     promoter        1. .362
                     /note="CMV IE1; similar to GenBank Accession Number
                     X03922"
     TATA_signal     329. .333
     misc_feature    356
                     /note="transcription start site"
     misc_feature    372. .428
                     /note="multiple cloning site"
     misc_feature    431. .576
                     /note="portion of SV40 genome; similar to GenBank
                     Accession Number J02400"
     misc_feature    572. .866
                     /note="portion of SV40 genome; similar to GenBank
                     Accession Number J02400"
     polyA_signal    763. .768
                     /note="SV40"
     polyA_signal    792. .797
                     /note="SV40"
     misc_feature    881. .1096
                     /note="portion of adenovirus type 5 genome; similar to
                     GenBank Accession Number X02996"
ORIGIN

  Query Match            94.6%;  Score 210;  DB 11;  Length 1096;
  Best Local Similarity  99.1%;  Pred. No. 1.6e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 701

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        702 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 761

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 821

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        822 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 865


Search completed: November 21, 2005, 23:21:27
Job time : 1904.45 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:49:24 ; Search time 335.836 Seconds
(without alignments)
4405.602 Million cell updates/sec

Title: US-10-683-775-3
Perfect score: 222
Sequence: 1 accacatttgtagaggtttt.....gtatcttatcatgtctggat 222

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	222	100.0	222	5	AAF30815	Aaf30815 SV40 late
	2	222	100.0	222	5	AAF30816	Aaf30816 SV40 earl
c	3	210	94.6	250	8	ADA50602	Ada50602 SV40 poly
c	4	210	94.6	667	5	AAD04943	Aad04943 Insert se
c	5	210	94.6	677	2	AAT97157	Aat97157 SV40 poly
	6	210	94.6	717	3	AAA74636	Aaa74636 Plasmid p
c	7	210	94.6	770	5	AAD04942	Aad04942 Insert se
	8	210	94.6	782	5	AAH20736	Aah20736 SV40 DNA
	9	210	94.6	816	14	ADV21047	Adv21047 4x-Polyad
	10	210	94.6	816	14	ADY66741	Ady66741 4X-polyad
c	11	210	94.6	1193	6	AAL42929	Aal42929 Medaka ov
c	12	210	94.6	1223	4	AAL02861	Aal02861 Human rep
c	13	210	94.6	1359	4	AAS41785	Aas41785 Genomic s
c	14	210	94.6	1359	4	AAS41797	Aas41797 Genomic s
c	15	210	94.6	1359	4	AAS41878	Aas41878 Genomic s
c	16	210	94.6	1359	4	AAS41845	Aas41845 Genomic s
c	17	210	94.6	1359	4	AAS41831	Aas41831 Genomic s
c	18	210	94.6	1359	4	AAS41894	Aas41894 Genomic s
c	19	210	94.6	1359	4	AAK85458	Aak85458 Human imm
c	20	210	94.6	1359	4	AAK85525	Aak85525 Human imm
c	21	210	94.6	1359	4	AAK85475	Aak85475 Human imm
c	22	210	94.6	1359	4	AAK69632	Aak69632 Human imm
c	23	210	94.6	1359	4	AAK85508	Aak85508 Human imm
c	24	210	94.6	1359	4	AAK69645	Aak69645 Human imm
c	25	210	94.6	1359	4	AAL02859	Aal02859 Human rep
c	26	210	94.6	1359	4	AAL02903	Aal02903 Human rep
c	27	210	94.6	1359	4	AAL02870	Aal02870 Human rep
c	28	210	94.6	1362	4	AAS41789	Aas41789 Genomic s
c	29	210	94.6	1362	4	AAS41882	Aas41882 Genomic s
c	30	210	94.6	1362	4	AAS41833	Aas41833 Genomic s
c	31	210	94.6	1362	4	AAK69636	Aak69636 Human imm
c	32	210	94.6	1362	4	AAK85462	Aak85462 Human imm
c	33	210	94.6	1362	4	AAK85512	Aak85512 Human imm
c	34	210	94.6	1362	4	AAL02864	Aal02864 Human rep
c	35	210	94.6	1423	4	AAS41787	Aas41787 Genomic s
c	36	210	94.6	1423	4	AAS41832	Aas41832 Genomic s
c	37	210	94.6	1423	4	AAS41880	Aas41880 Genomic s
c	38	210	94.6	1423	4	AAK69634	Aak69634 Human imm
c	39	210	94.6	1423	4	AAK85510	Aak85510 Human imm
c	40	210	94.6	1423	4	AAK85460	Aak85460 Human imm
c	41	210	94.6	1423	4	AAL02862	Aal02862 Human rep
c	42	210	94.6	1423	4	AAL02896	Aal02896 Human rep
c	43	210	94.6	1424	4	AAS41801	Aas41801 Genomic s
c	44	210	94.6	1424	4	AAS41853	Aas41853 Genomic s
c	45	210	94.6	1424	4	AAS41849	Aas41849 Genomic s

ALIGNMENTS

RESULT 1
AAF30815/c
ID AAF30815 standard; DNA; 222 BP.
XX
AC AAF30815;
XX
DT 21-JUN-2001 (first entry)
XX
DE SV40 late polyadenylation site.
XX
KW SV40; polyadenylation; vector; ss.
XX
OS Rhesus macaque polyoma virus.
XX
FH Key Location/Qualifiers
FT polyA_signal 123. .128
FT /*tag= a
FT misc_feature 151. .187
FT /*tag= b
FT /note= "G/T rich region"
XX
PN WO200127299-A1. ✓
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028431.
XX
PR 13-OCT-1999; 99US-0159177P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Mcgrew JT;
XX
DR WPI; 2001-290726/30.
XX
PT An expression vector for increasing the yield of recombinant protein
PT comprises a first protein operably linked to a second protein.
XX
PS Claim 4; Page 28; 41pp; English.
XX
CC The present sequence is that of the SV40 late polyadenylation site. This
CC SV40 late polyadenylation site, or nucleotides 80-222 of it, is utilised

CC in a claimed expression vector. The vector comprises a promoter sequence,
CC a first coding sequence, a polyadenylation site (preferably SV40 late or
CC early polyadenylation site), and a second coding sequence, preferably
CC encoding a selectable marker such as dihydrofolate reductase. The
CC internal polyadenylation site allows a single promoter to generate both
CC monocistronic messages and dicistronic messages. An internal ribosome
CC entry site (IRES) may be inserted between the internal polyadenylation
CC site and the DNA encoding the selectable marker. Similar, multicistronic
CC vectors can also be prepared. Cells transfected with the vector, and cell
CC lines cloned from them, are also claimed. These are used for obtaining a
CC recombinant protein in mammalian host cells. The expression vector is
CC useful as it comprises a selectable, amplifiable marker, while increasing
CC the proportion of mRNAs encoding a desired recombinant protein
XX
SQ Sequence 222 BP; 76 A; 30 C; 45 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 222; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 163

Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 103

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 43

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||
Db         42 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1
```

RESULT 2
AAF30816
ID AAF30816 standard; DNA; 222 BP.
XX
AC AAF30816;
XX
DT 21-JUN-2001 (first entry)
XX
DE SV40 early polyadenylation site.
XX
KW SV40; polyadenylation; vector; ss.
XX
OS Rhesus macaque polyoma virus.
XX
PN WO200127299-A1.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028431.
XX
PR 13-OCT-1999; 99US-0159177P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Mcgrew JT;
XX
DR WPI; 2001-290726/30.
XX
PT An expression vector for increasing the yield of recombinant protein
PT comprises a first protein operably linked to a second protein.
XX
PS Claim 4; Page 28-29; 41pp; English.
XX
CC The present sequence is that of the SV40 early polyadenylation site. This
CC SV40 early polyadenylation site can be utilised in a claimed expression
CC vector. The vector comprises a promoter sequence, a first coding
CC sequence, a polyadenylation site (preferably SV40 late or early
CC polyadenylation site), and a second coding sequence, preferably encoding
CC a selectable marker such as dihydrofolate reductase. The internal
CC polyadenylation site allows a single promoter to generate both
CC monocistronic messages and dicistronic messages. An internal ribosome
CC entry site (IRES) may be inserted between the internal polyadenylation
CC site and the DNA encoding the selectable marker. Similar, multicistronic
CC vectors can also be prepared. Cells transfected with the vector, and cell
CC lines cloned from them, are also claimed. These are used for obtaining a
CC recombinant protein in mammalian host cells. The expression vector is
CC useful as it comprises a selectable, amplifiable marker, while increasing
CC the proportion of mRNAs encoding a desired recombinant protein
XX
SQ Sequence 222 BP; 71 A; 45 C; 30 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 222; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60

Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||
Db        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
```

RESULT 3
ADA50602/c
ID ADA50602 standard; DNA; 250 BP.
XX
AC ADA50602;
XX
DT 20-NOV-2003 (first entry)
XX
DE SV40 polyadenylation signal (late and early), SEQ ID NO:57.
XX
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
KW humoral response; cellular response; immune response; immunotherapy;
KW cancer; cytostatic; vaccine; gene therapy; SV40; ds.
XX
OS Simian virus 40.
XX
PN WO2003031569-A2.
XX
PD 17-APR-2003.
XX
PF 18-SEP-2002; 2002WO-US029640.
XX
PR 10-OCT-2001; 2001US-0328371P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;
PI Branigan PJ;
XX
DR WPI; 2003-393437/37.
XX
PT New nucleic acid vaccine, useful for eliciting an immune response to a
PT cancer associated tumor protein in a mammal.
XX
PS Disclosure; Page 50; 92pp; English.
XX
CC The invention relates to a nucleic acid vaccine comprising one or more

CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,
CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
CC is preferably under the control of a promoter such as the cytomegalovirus
CC immediate early promoter, the dihydrofoliate reductase promoter or the
CC early or late SV40 promoters. The invention also encompasses the method
CC of eliciting an immune response to a tumour antigen in a mammal using the
CC vaccine of the invention. Coexpression of the antigen and adjuvant
CC induces a humoral or cellular response to the tumour antigen, generating
CC an immune reponse useful for treatment or prophylaxis of cancers. The
CC present sequence represents a regulatory nucleic acid used in DNA vaccine
CC vectors of the invention.
XX
SQ Sequence 250 BP; 85 A; 33 C; 54 G; 78 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 8; Length 250;
Best Local Similarity 99.1%; Pred. No. 2.6e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 169

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        168 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 109

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 49

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         48 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 5
```

RESULT 4
AAD04943/c
ID AAD04943 standard; DNA; 667 BP.
XX
AC AAD04943;
XX
DT 17-JUL-2001 (first entry)
XX
DE Insert sequence in pRK80c plasmid.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; pRK80c plasmid; ds.
XX
OS Unidentified.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Example 2; Page 65; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific
CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene
CC trapping construct is useful for mutationally inactivating all cellular
CC genes. The present sequence is an insert sequence in plasmid pRK80c. The
CC insert sequence is the Cre or C31-Int mediated inversion product. The
CC pRK80b is used for sequencing the Cre or C31-Int mediated inversion
CC product
XX
SQ Sequence 667 BP; 180 A; 156 C; 157 G; 173 T; 0 U; 1 Other;

Query Match 94.6%; Score 210; DB 5; Length 667;
Best Local Similarity 99.1%; Pred. No. 3.2e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 493

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        492 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 433

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 373

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        372 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 329
```

RESULT 5
AAT97157/c
ID AAT97157 standard; DNA; 677 BP.
XX
AC AAT97157;
XX
DT 11-MAY-1998 (first entry)
XX
DE SV40 poly A signal.
XX
KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
KW gene amplification; immunotherapy; therapy; SV40; poly A signal; ds.
XX
OS Rhesus macaque polyoma virus.
XX
PN WO9741244-A1.
XX
PD 06-NOV-1997.
XX
PF 25-APR-1997; 97WO-US007039.
XX
PR 01-MAY-1996; 96US-00644664.
PR 06-DEC-1996; 96US-00761277.
XX
PA (GENI-) GENITOPE CORP.
XX
PI Denney DW;

XX
DR WPI; 1997-549743/50.
XX
PT Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at
PT least 2 different recombinant variable regions of immunoglobulin
PT molecules derived from B cell lymphoma cells.
XX
PS Disclosure; Page 103; 177pp; English.
XX
CC This genomic DNA fragment comprises the SV40 poly A signal. It is used as
CC a regulatory element in expression vectors designed for efficient
CC expression of genes in eukaryotic cells. The invention provides vectors
CC and improved methods for the expression and co-amplification of genes
CC encoding recombinant proteins in cultured cells. The methods permit the
CC isolation of cell lines which have co-amplified input recombinant
CC sequences which encode an amplifiable marker, one or more expression
CC vectors encoding a protein of interest and optionally a selectable
CC marker. The amplified cells provide large quantities of recombinant
CC proteins suitable for immunotherapy for treatment of lymphomas and
CC leukaemias. The methods permit the production of custom vaccines,
CC including multivalent vaccines that reflect the degree of somatic
CC variation found in a patient's tumour
XX
SQ Sequence 677 BP; 202 A; 144 C; 112 G; 219 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 2; Length 677;
Best Local Similarity 99.1%; Pred. No. 3.2e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 167

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        166 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 107

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 47

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         46 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3
```

RESULT 6
AAA74636
ID AAA74636 standard; DNA; 717 BP.
XX
AC AAA74636;
XX
DT 05-DEC-2000 (first entry)
XX
DE Plasmid pNSE-p25 3' UTR and SV40 polyadenylation sequence.
XX
KW p25; cdk5 activator; SV40 polyadenylation signal; untranslated region;
KW UTR; neuron specific enolase; NSE; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; amyelolateral sclerosis;
KW Huntington's disease; traumatic brain injury; stroke; transgenic animal;
KW spinocerebellar degeneration; tau hyperphosphorylation; ds.
XX
OS Rous sarcoma virus.
XX
PN EP1026251-A2.
XX
PD 09-AUG-2000.
XX
PF 02-FEB-2000; 2000EP-00300797.
XX
PR 03-FEB-1999; 99US-0118478P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Ahlijanian MK, Mcneish JD;
XX
DR WPI; 2000-507252/46.
XX
PT New recombinant DNA molecule comprising gene encoding p25, useful for
PT producing transgenic animal to serve as model for Alzheimer's-associated
PT neurofibrillary tangle formation.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The present sequence is the 3' untranslated region (UTR) and SV40
CC polyadenylation signal sequence of plasmid NSE-p25. The plasmid also
CC contains the human cDNA for p25, an activator of the protein kinase cdk5,
CC operably linked to the rat neuron specific enolase (NSE) promoter. The
CC NSE-p25 transgene was used in the production of transgenic mice
CC overexpressing human p25. Overexpression of p25 is sufficient to produce
CC hyperphosphorylation of tau, which is seen in the neurofibrillary tangles
CC associated with Alzheimer's disease. The transgenic animals are useful as
CC in vivo systems for screening potential therapeutic compounds for their
CC ability to inhibit or prevent the production of hyperphosphorylated tau
CC and associated neuronal death. The transgenic animals are suitable for
CC use as disease models of neurodegenerative diseases and tau-related
CC pathologies, such as Alzheimer's disease, Parkinson's disease,
CC amyelolateral sclerosis, Huntington's disease, stroke, traumatic brain
CC injury, spinocerebellar degeneration. They are also useful as models of
CC cdk5/p25 and tau biochemistry, and to establish the role of the human p25
CC in the formation of hyperphosphorylated tau in neurodegenerative
CC conditions
XX
SQ Sequence 717 BP; 229 A; 129 C; 131 G; 228 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 3; Length 717;
Best Local Similarity 99.1%; Pred. No. 3.2e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 551

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        552 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 611

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 671

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        672 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 715
```

RESULT 7
AAD04942/c
ID AAD04942 standard; DNA; 770 BP.
XX
AC AAD04942;
XX
DT 17-JUL-2001 (first entry)
XX
DE Insert sequence in pRK80b plasmid.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; pRK80b plasmid; ds.
XX
OS Unidentified.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX

```
PF   16-OCT-2000; 2000WO-EP010162.
XX
PR   16-OCT-1999;   99EP-00120592.
PR   27-OCT-1999;   99US-0162016P.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
PA   (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI   Kuehn R,  Von Melchener H,  Altschmied J;
XX
DR   WPI; 2001-308486/32.
XX
PT   New gene trapping construct capable of causing conditional mutations in
PT   genes, comprises functional DNA segment inserted in sense or antisense
PT   direction relative to gene to be trapped.
XX
PS   Example 2; Page 65; 78pp; English.
XX
CC   The present invention relates to a conditional gene trapping construct
CC   capable of causing conditional mutations in genes. The gene trapping
CC   construct comprises two functional DNA segments, each being flanked by
CC   two recombinase recognition sequences (RRSs) specific to site specific
CC   recombinase which is capable of unidirectional inversion of double
CC   standard DNA segment. One of the DNA segment (disruption cassette) is
CC   inserted in antisense orientation relative to the transcriptional
CC   orientation of the gene to be trapped. The other DNA segment (selection
CC   cassette) is inserted in sense direction relative to the transcriptional
CC   orientation of the gene to be trapped. The cell comprising the gene
CC   trapping construct is useful for the identification and/or isolation of
CC   genes. The transgenic organism comprising the gene trapping construct is
CC   useful to study gene function at various developmental stages. The gene
CC   trapping construct is useful for mutationally inactivating all cellular
CC   genes. The present sequence is an insert sequence in plasmid pRK80b. The
CC   insert sequence is the Cre or C31-Int mediated inversion product. The
CC   pRK80b is used for sequencing the Cre or C31-Int mediated inversion
CC   product
XX
SQ   Sequence 770 BP; 208 A; 199 C; 174 G; 188 T; 0 U; 1 Other;

  Query Match             94.6%;  Score 210;  DB 5;  Length 770;
  Best Local Similarity   99.1%;  Pred. No. 3.3e-43;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 599

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        598 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 539

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 479

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        478 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 435


RESULT 8
AAH20736
ID   AAH20736 standard; DNA; 782 BP.
XX
AC   AAH20736;
XX
DT   13-AUG-2001  (first entry)
XX
DE   SV40 DNA fragment.
XX
KW   Gene therapy; amniocyte; cytostatic; Ad5; E1A region; E1B region;
KW   modified tropism; tumor; ss.
XX
OS   Rhesus macaque polyoma virus.
XX
PN   WO200136615-A2.
XX
PD   25-MAY-2001.
XX
PF   07-NOV-2000; 2000WO-EP010992.
XX
PR   18-NOV-1999;   99DE-01055558.
XX
PA   (KOCH/) KOCHANEK S.
XX
PI   Kochanek S,  Schiedner G;
XX
DR   WPI; 2001-343817/36.
XX
PT   New permanent amniocyte cell lines, useful for producing viral gene
PT   therapy vectors or mutant adenoviruses, express the adenoviral E1A and
PT   E1B gene products.
XX
PS   Example 1; Page 64; 72pp; German.
XX
CC   This invention describes novel permanent amniocyte cell lines (A),
CC   containing at least one nucleic acid (I) that causes expression of the
CC   gene products (II) of the adenoviral E1A and E1B regions. (A) are used to
CC   produce gene therapy vectors, especially adeno, adeno-associated, retro
CC   or lenti viral vectors, particularly first- or second generation, large-
CC   capacity or deleted adenoviral vectors. (A) are also used to produce
CC   adenoviral mutants, optionally with modified tropism. The vectors may
CC   express a wide range of therapeutic proteins or antisense RNAs.
CC   Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
CC   for treating tumors, they replicate in the cells but not significantly in
CC   normal primary cells. (A) can be made efficiently, simply and
CC   reproducibly. The products of the invention have cytostatic activity.
CC   This sequence represents a DNA fragment derived from SV40 which is
CC   described in the method of the invention
XX
SQ   Sequence 782 BP; 250 A; 137 C; 134 G; 261 T; 0 U; 0 Other;

  Query Match             94.6%;  Score 210;  DB 5;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 3.3e-43;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 611

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        612 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 671

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 731

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        732 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 775


RESULT 9
ADV21047
ID   ADV21047 standard; DNA; 816 BP.
XX
AC   ADV21047;
XX
DT   24-FEB-2005  (first entry)
XX
DE   4x-Polyadenylation element DNA.
XX
KW   Genetic engineering; gene targeting; gene trapping;
KW   internal ribosomal entry site; IRES; IGS; inducible gene silencer; ds.
XX
```

OS Unidentified.
XX
PN US2004241851-A1.
XX
PD 02-DEC-2004.
XX
PF 30-MAY-2003; 2003US-00448395.
XX
PR 30-MAY-2003; 2003US-00448395.
XX
PA (AMHP) WYETH.
XX
PI Askew GR, Kanki KL;
XX
DR WPI; 2005-011640/01.
XX
PT New inducible gene silencer, useful for conditionally knocking out and
PT altering gene function and genetic sequences, and for gene trapping and
PT targeting.
XX
PS Claim 8; SEQ ID NO 7; 41pp; English.
XX
CC The present invention relates to an inducible gene silencer comprising a
CC splice acceptor sequence, an internal ribosomal entry site (IRES)
CC sequence, a nucleotide sequence coding for a reporter protein, a
CC polyadenylation sequence and a pair of oppositely oriented recombination
CC site sequences, which cause single cycle inversions in the presence of a
CC suitable recombinase enzyme, flanking the elements cited above. The
CC invention is useful for conditionally knocking out and altering gene
CC function and genetic sequences and for gene trapping and targeting. The
CC present sequence is a 4x-Polyadenylation (4x-PolyA) element DNA. This
CC element DNA is used to construct the inducible gene siliencer (IGS).
XX
SQ Sequence 816 BP; 257 A; 169 C; 122 G; 268 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 14; Length 816;
Best Local Similarity 99.1%; Pred. No. 3.3e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 146

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        147 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 206

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 266

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        267 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 310
```

RESULT 10
ADY66741
ID ADY66741 standard; DNA; 816 BP.
XX
AC ADY66741;
XX
DT 19-MAY-2005 (first entry)
XX
DE 4X-polyadenylation sequence (4X-PolyA) SEQ ID NO:7.
XX
KW knockout gene trapping; gene targeting; inducible gene silencer; ds.
XX
OS Synthetic.
XX
PN CA2428972-A1.
XX
PD 30-NOV-2004.
XX
PF 30-MAY-2003; 2003CA-02428972.
XX
PR 30-MAY-2003; 2003CA-02428972.
XX
PA (AMHP) WYETH.
XX
PI Barton M, Askew GR, Kanki KL;
XX
DR WPI; 2005-049264/06.
XX
PT Conditional knockout gene targeting, involves transfecting vector
PT comprising gene silencer into host cell, delivering suitable recombinase
PT enzyme to host cell, to cause inducible gene silencer to invert into
PT active orientation.
XX
PS Claim 8; SEQ ID NO 7; 60pp; English.
XX
CC The invention relates to a method for conditional knockout gene trapping
CC or gene targeting. The method comprises: (a) preparing an inducible gene
CC silencer comprising a splice acceptor sequence, an internal ribosomal
CC entry site (IRES) sequence, a nucleotide sequence coding for a reporter
CC protein, a polyadenylation sequence, and a pair of oppositely oriented
CC recombination site sequences which cause single cycle inversions in the
CC presence of a suitable recombinase enzyme; (b) flanking the previously
CC identified elements; (c) inserting the inducible gene silencer into a
CC vector in an inert orientation; (d) transfecting the vector comprising
CC the inducible gene silencer into a host cell; and (e) delivering a
CC suitable recombinase enzyme to the host cell or to any organism deriving
CC from the host cell, at any desired time, to cause the inducible gene
CC silencer to invert into an active orientation, so that the inducible gene
CC silencer knocks out the functioning of a gene into which it has inserted
CC and expresses the reporter protein. The present sequence represents a 4X-
CC polyadenylation sequence (4X-PolyA) which can be used in an inducible
CC gene silencer from the present invention.
XX
SQ Sequence 816 BP; 257 A; 169 C; 122 G; 268 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 14; Length 816;
Best Local Similarity 99.1%; Pred. No. 3.3e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 146

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        147 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 206

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 266

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        267 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 310
```

RESULT 11
AAL42929/c
ID AAL42929 standard; DNA; 1193 BP.
XX
AC AAL42929;
XX
DT 06-AUG-2002 (first entry)
XX
DE Medaka ovarian cytochrome P450 aromatase gene and promoter sequence.
XX
KW Medaka; Japanese rice fish; gene; ds; phenotypic sex modification;
KW ovarian cytochrome P450 aromatase promoter; blocker molecule;
KW ovarian P450 aromatase; sexual development; single sex line production;
KW pest eradication.

XX
OS Oryzias latipes.
XX
PN WO200230183-A1.
XX
PD 18-APR-2002.
XX
PF 09-OCT-2001; 2001WO-AU001264.
XX
PR 09-OCT-2000; 2000AU-00000646.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Thresher R, Hinds L, Grewe P, Patil J;
XX
DR WPI; 2002-416816/44.
XX
PT Novel construct for modifying phenotypic sex in animals to distort
PT operational sex ratio of exotic pests, comprises a promoter activated
PT during sex-determining stage and blocker that alters normal sexual
PT development.
XX
PS Claim 9; Page 97-98; 121pp; English.
XX
CC The invention comprises a construct for modifying phenotypic sex in
CC animals. The construct contains a promoter (i.e. a medaka ovarian
CC cytochrome P450 aromatase promoter). The promoter is operably linked to a
CC second nucleic acid encoding a blocker molecule (i.e. medaka or zebrafish
CC ovarian P450 aromatase) that alters normal sexual development in the
CC animal. The construct is useful for altering phenotypic sex in animals
CC (e.g. fish). The construct is also useful in animal husbandry in
CC producing single sex lines and can therefore be used to distort the
CC operational sex ratio - leading to reproductive failure, population
CC decline and eradication of a pest population. The construct can also be
CC used to alter sexual development in animals which induces sterility or
CC modifies phenotypic sex. The present DNA sequence represents the medaka
CC ovarian cytochrome P450 aromatase gene and promoter sequence
XX
SQ Sequence 1193 BP; 341 A; 260 C; 276 G; 316 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 6; Length 1193;
Best Local Similarity 99.1%; Pred. No. 3.5e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 1067

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1066 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1007

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 947

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        946 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 903
```

RESULT 12
AAL02861/c
ID AAL02861 standard; DNA; 1223 BP.
XX
AC AAL02861;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5549.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001339.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465570/50.
XX
PT   Isolated nucleic acid molecule encoding a reproductive system antigen is
PT   used in preventing, treating or ameliorating a medical condition.
XX
PS   Disclosure; SEQ ID NO 5549; 1297pp + Sequence Listing; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human reproductive system related antigens. These can be used
CC   in the prevention and treatment of reproductive system disorders,
CC   including cancer. The present sequence is a genomic sequence encoding a
CC   protein of the invention
XX
SQ   Sequence 1223 BP; 363 A; 255 C; 264 G; 340 T; 0 U; 1 Other;

  Query Match             94.6%;  Score 210;  DB 4;  Length 1223;
  Best Local Similarity   99.1%;  Pred. No. 3.5e-43;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 166

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        165 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 106

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 46

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         45 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 2


RESULT 13
AAS41785/c
ID   AAS41785 standard; DNA; 1359 BP.
XX
AC   AAS41785;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Genomic sequence #101 encoding novel human enzyme polypeptide.
XX
KW   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW   anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155301-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001239.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
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PR   02-MAR-2000; 2000US-0186350P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 17-NOV-2000; 2000US-0249300P.
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PR 01-DEC-2000; 2000US-0250391P.
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PR 06-DEC-2000; 2000US-0251479P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Disclosure; SEQ ID NO 1911; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the

```
CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC   DNA sequences encoding for the novel human enzyme polypeptides of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1359 BP; 395 A; 301 C; 303 G; 360 T; 0 U; 0 Other;

  Query Match             94.6%;  Score 210;  DB 4;  Length 1359;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-43;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 165

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        164 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 105

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 45

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         44 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1


RESULT 14
AAS41797/c
ID   AAS41797 standard; DNA; 1359 BP.
XX
AC   AAS41797;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Genomic sequence #113 encoding novel human enzyme polypeptide.
XX
KW   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW   anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155301-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001239.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
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PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
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PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
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PR   22-AUG-2000; 2000US-0226868P.
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PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
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PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465566/50.
XX
PT   Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT   treating neural, immune system, muscular, reproductive, pulmonary,
PT   cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS   Disclosure; SEQ ID NO 1923; 1180pp; English.
XX
CC   The present invention relates to the isolation of novel human enzyme
CC   polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC   encoding them. The enzyme polypeptides of the invention may comprise the
CC   functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC   isomerases or ligases. The sequences of the invention are useful in the
CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC   DNA sequences encoding for the novel human enzyme polypeptides of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
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KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW   anti arthritic; nephrotropic; anticoagulant; ds.
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OS   Homo sapiens.
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PN   WO200155301-A2.
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PD   02-AUG-2001.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Disclosure; SEQ ID NO 2004; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders

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CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC   DNA sequences encoding for the novel human enzyme polypeptides of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
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SQ   Sequence 1359 BP; 395 A; 301 C; 303 G; 360 T; 0 U; 0 Other;

  Query Match             94.6%;  Score 210;  DB 4;  Length 1359;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-43;
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ALIGNMENTS

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AUTHORS Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A., Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
TITLE Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rerio embryonic library
JOURNAL Unpublished (2003)
COMMENT Contact: Chen F.
Exelixis, Inc.
170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
Tel: 650 837 7000
Fax: 650 837 8300
Email: fchen@exelixis.com
DNA Sequencing by: Exelixis, Inc. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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ORIGIN

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  Query Match            94.6%;  Score 210;  DB 6;  Length 278;
  Best Local Similarity  99.1%;  Pred. No. 3.1e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 93

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         94 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 153

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 213

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        214 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 257


RESULT 2
CV006397
LOCUS       CV006397                334 bp    mRNA    linear   EST 18-AUG-2004
DEFINITION  CS_gil_12H12_M13Reverse Blue crab gill, normalized Callinectes
            sapidus cDNA clone CS_gil_12H12 5' similar to prf|1103278B ORF.
            Score = 89.0 bits (219), Expect = 3e-17, mRNA sequence.
ACCESSION   CV006397
VERSION     CV006397.1  GI:51365620
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 12  row: H  column: 12
            Seq primer: M13 Reverse
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_gil_12H12"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match            94.6%;  Score 210;  DB 7;  Length 334;
  Best Local Similarity  99.1%;  Pred. No. 3.1e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 138

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        139 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 198

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 258

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        259 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 302


RESULT 3
CD279996
LOCUS       CD279996                353 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43757.10 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6321722 5',
            mRNA sequence.
ACCESSION   CD279996
VERSION     CD279996.1  GI:31057772
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 353)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13762  row: C  column: 3
            High quality sequence stop: 353.
FEATURES             Location/Qualifiers
     source          1. .353
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6321722"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            94.6%;  Score 210;  DB 6;  Length 353;
  Best Local Similarity  99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;
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Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 141

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        142 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 201

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 261

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        262 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 305
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RESULT 4
AL039087
LOCUS       AL039087                372 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566H204_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566H204 3', mRNA sequence.
ACCESSION   AL039087
VERSION     AL039087.1  GI:5408188
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Bloecker, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 3' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No r1 sequence available.
            This clone (DKFZp566H204) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566H204"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 1;  Length 372;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 193

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        194 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 253

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 313

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        314 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 357
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RESULT 5
CV161679
LOCUS       CV161679                380 bp    mRNA    linear   EST 08-SEP-2004
DEFINITION  CS_gil_54H02_M13Reverse Blue crab gill, normalized Callinectes
            sapidus cDNA clone CS_gil_54H02 5' similar to prf|1103278B ORF.
            Score = 60.8 bits (146), Expect = 9e-09, mRNA sequence.
ACCESSION   CV161679
VERSION     CV161679.1  GI:51946943
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 54  row: H  column: 02
            Seq primer: M13 Reverse
            High quality sequence stop: 350.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_gil_54H02"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 7;  Length 380;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 90

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
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                ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          91 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 150

Qy         119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 210

Qy         179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
                |||||||||||||||||||||||||||||||||||||||||||
Db         211 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 254


RESULT 6
BP420484/c
LOCUS       BP420484                 395 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420484 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE03774r 3', mRNA sequence.
ACCESSION   BP420484
VERSION     BP420484.1  GI:66786737
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE03774r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 395;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 208

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        207 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 148

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 88

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         87 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 44


RESULT 7
CD281635
LOCUS       CD281635                 429 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43981.18 NCI_CGAP_ZEmb2 Danio rerio cDNA clone IMAGE:6319444 5',
            mRNA sequence.
ACCESSION   CD281635
VERSION     CD281635.1  GI:31059411
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13756  row: D  column: 5
            High quality sequence stop: 429.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6319444"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb2"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 429;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 198

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        199 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 258

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 318

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        319 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 362


RESULT 8
CV527659
LOCUS       CV527659                 430 bp    mRNA    linear   EST 07-OCT-2004
DEFINITION  CS_GIL_06H06_SP6 Blue crab gill, normalized Callinectes sapidus
            cDNA clone CS_GIL_06H06 5' similar to prf|1103278B ORF. Score =
            89.0 bits (219), Expect = 3e-17, mRNA sequence.
ACCESSION   CV527659
VERSION     CV527659.1  GI:53912038
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
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            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biolbgical Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 06  row: H  column: 06
            Seq primer: SP6
            High quality sequence start: 7
            High quality sequence stop: 406.
FEATURES             Location/Qualifiers
     source          1. .430
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_GIL_06H06"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 7;  Length 430;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 265

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        266 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 325

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 385

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        386 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 429


RESULT 9
BP426053/c
LOCUS       BP426053                 431 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP426053 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE09943r 3', mRNA sequence.
ACCESSION   BP426053
VERSION     BP426053.1  GI:66792306
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE09943r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 431;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 271

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        270 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 211

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 151

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        150 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 107


RESULT 10
BP418262/c
LOCUS       BP418262                 455 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP418262 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE01346r 3', mRNA sequence.
ACCESSION   BP418262
VERSION     BP418262.1  GI:66784515
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Homo sapiens"
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE01346r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 455;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        291 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 232

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        231 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 172

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 112

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        111 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 68


RESULT 11
BP418191/c
LOCUS       BP418191                461 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP418191 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE01271r 3', mRNA sequence.
ACCESSION   BP418191
VERSION     BP418191.1  GI:66784444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .461
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE01271r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 461;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        326 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 267

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        266 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 207

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 147

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        146 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 103


RESULT 12
CD280357
LOCUS       CD280357                464 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43757.71 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6321976 5',
            mRNA sequence.
ACCESSION   CD280357
VERSION     CD280357.1  GI:31058133
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 464)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13762  row: M  column: 17
            High quality sequence stop: 464.
FEATURES             Location/Qualifiers
     source          1. .464
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6321976"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 464;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db         18 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 77

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         78 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 137

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 197

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db        198 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 241


RESULT 13
CV526695
LOCUS       CV526695                495 bp    mRNA    linear   EST 07-OCT-2004
DEFINITION  CS_GIL_17C02_SP6 Blue crab gill, normalized Callinectes sapidus
            cDNA clone CS_GIL_17C02 5' similar to prf|1103278B ORF. Score =
            89.0 bits (219), Expect = 4e-17, mRNA sequence.
ACCESSION   CV526695
VERSION     CV526695.1  GI:53911074
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 17  row: C  column: 02
            Seq primer: SP6
            High quality sequence start: 3
            High quality sequence stop: 378.
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     source          1. .495
                     /organism="Callinectes sapidus"
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                     /clone="CS_GIL_17C02"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match            94.6%;  Score 210;  DB 7;  Length 495;
  Best Local Similarity  99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        136 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 195

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        196 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 255

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        256 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 315

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        316 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 359


RESULT 14
BP420735/c
LOCUS       BP420735                503 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420735 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE04048r 3', mRNA sequence.
ACCESSION   BP420735
VERSION     BP420735.1  GI:66786988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 503)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .503
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE04048r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match            94.6%;  Score 210;  DB 3;  Length 503;
  Best Local Similarity  99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 261

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        260 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 201

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 141

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        140 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 97


RESULT 15
BP420280/c
LOCUS       BP420280                507 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420280 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE03560r 3', mRNA sequence.
ACCESSION   BP420280
VERSION     BP420280.1  GI:66786533
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE03560r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 507;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        393 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 334

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        333 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 274

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db        273 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 214

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db        213 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 170


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:57:15 ; Search time 100.221 Seconds
(without alignments)
3937.467 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	222	100.0	222	3	US-09-687-050-1	Sequence 1, Appli
	2	222	100.0	222	3	US-09-687-050-3	Sequence 3, Appli
c	3	210	94.6	677	2	US-08-644-664B-3	Sequence 3, Appli
c	4	210	94.6	677	2	US-08-761-277A-3	Sequence 3, Appli
	5	210	94.6	717	3	US-09-496-445-3	Sequence 3, Appli
	6	210	94.6	782	3	US-09-714-550-8	Sequence 8, Appli
	7	210	94.6	2792	3	US-08-994-689C-8	Sequence 8, Appli
	8	210	94.6	3218	3	US-09-496-445-4	Sequence 4, Appli
	9	210	94.6	3318	3	US-08-169-613A-1	Sequence 1, Appli
c	10	210	94.6	3740	3	US-08-955-565A-6	Sequence 6, Appli
	11	210	94.6	3822	3	US-08-675-566-8	Sequence 8, Appli
	12	210	94.6	3944	2	US-07-678-408A-1	Sequence 1, Appli
	13	210	94.6	3955	3	US-08-675-566-10	Sequence 10, Appl
	14	210	94.6	4009	3	US-08-675-566-9	Sequence 9, Appli
c	15	210	94.6	4059	2	US-08-564-313-2	Sequence 2, Appli
c	16	210	94.6	4059	6	PCT-US94-06069-2	Sequence 2, Appli
	17	210	94.6	4273	3	US-08-795-430-3	Sequence 3, Appli
	18	210	94.6	4273	3	US-09-355-700-3	Sequence 3, Appli
	19	210	94.6	4273	3	US-08-601-132-37	Sequence 37, Appl
	20	210	94.6	4273	3	US-08-671-573B-37	Sequence 37, Appl
	21	210	94.6	4273	3	US-09-631-092B-37	Sequence 37, Appl
	22	210	94.6	4273	3	US-09-534-376A-3	Sequence 3, Appli
c	23	210	94.6	4455	2	US-08-474-169-5	Sequence 5, Appli
	24	210	94.6	4503	3	US-08-675-566-7	Sequence 7, Appli
	25	210	94.6	4776	3	US-09-287-368-7	Sequence 7, Appli
	26	210	94.6	4810	2	US-08-188-281B-3	Sequence 3, Appli
	27	210	94.6	4810	2	US-08-453-552-7	Sequence 7, Appli
	28	210	94.6	4810	2	US-08-710-637-7	Sequence 7, Appli
	29	210	94.6	4810	6	PCT-US93-00907-7	Sequence 7, Appli
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c	34	210	94.6	4963	2	US-08-481-970-9	Sequence 9, Appli
c	35	210	94.6	4963	2	US-08-897-719-9	Sequence 9, Appli
c	36	210	94.6	4963	3	US-09-163-269-9	Sequence 9, Appli
c	37	210	94.6	4963	3	US-09-281-674-9	Sequence 9, Appli
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	40	210	94.6	5030	2	US-08-588-201-14	Sequence 14, Appl
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	42	210	94.6	5030	3	US-08-893-327-14	Sequence 14, Appl
	43	210	94.6	5067	3	US-08-675-566-20	Sequence 20, Appl
	44	210	94.6	5125	2	US-08-453-552-11	Sequence 11, Appl
	45	210	94.6	5125	2	US-08-710-637-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-687-050-1/c
; Sequence 1, Application US/09687050
; Patent No. 6632637
; GENERAL INFORMATION:
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: VECTORS AND METHODS FOR RECOMBINANT PROTEIN EXPRESSION
; FILE REFERENCE: 2902-A
; CURRENT APPLICATION NUMBER: US/09/687,050
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,177
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 222
; TYPE: DNA
; ORGANISM: SV40
US-09-687-050-1

Query Match 100.0%; Score 222; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 8.1e-50;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AAACATAAAATGAATGCAATTGTTGTTGAACTTGTTTATTGCAGCTTATAATGGTTACAA 103

Qy        121 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG 43

Qy        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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RESULT 2
US-09-687-050-3
; Sequence 3, Application US/09687050
; Patent No. 6632637
; GENERAL INFORMATION:
; APPLICANT: McGrew, Jeffrey T.

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;  TITLE OF INVENTION:   VECTORS AND METHODS FOR RECOMBINANT PROTEIN EXPRESSION
;  FILE REFERENCE:   2902-A
;  CURRENT APPLICATION NUMBER: US/09/687,050
;  CURRENT FILING DATE:  2000-10-12
;  PRIOR APPLICATION NUMBER:   60/159,177
;  PRIOR FILING DATE:   1999-10-13
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 222
;   TYPE: DNA
;   ORGANISM: SV40
US-09-687-050-3

  Query Match             100.0%;  Score 222;  DB 3;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-50;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        181 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222


RESULT 3
US-08-644-664B-3/c
; Sequence 3, Application US/08644664B
; Patent No. 5776746
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Gene Amplication Methods
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/644,664B
;      FILING DATE:  01-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  GENITOPE-00912
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  677 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-644-664B-3

  Query Match             94.6%;  Score 210;  DB 2;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 167

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        166 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 107

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 47

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         46 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3


RESULT 4
US-08-761-277A-3/c
; Sequence 3, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  677 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-761-277A-3

  Query Match             94.6%;  Score 210;  DB 2;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        226 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 167

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        166 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 107

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db        106 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 47

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db         46 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3


RESULT 5
US-09-496-445-3
; Sequence 3, Application US/09496445
; Patent No. 6693226
; GENERAL INFORMATION:
;  APPLICANT: McNeish, John D.
;  APPLICANT: Ahlijnian, Michael K
;  TITLE OF INVENTION: Transgenic Animals Expressing Human p25
;  FILE REFERENCE: PC10142A
;  CURRENT APPLICATION NUMBER: US/09/496,445
;  CURRENT FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Rous sarcoma virus
US-09-496-445-3

  Query Match             94.6%;  Score 210;  DB 3;  Length 717;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Db        492 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 551

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
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Db        552 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 611

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db        612 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 671

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db        672 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 715


RESULT 6
US-09-714-550-8
; Sequence 8, Application US/09714550
; Patent No. 6558948
; GENERAL INFORMATION:
;  APPLICANT: Kochanek, Stefan
;  APPLICANT:  Schiedner, Gudrun
;  TITLE OF INVENTION: Permanent amniocytic cell line, its
;  TITLE OF INVENTION:  production and use for the production of gene transfer
;  TITLE OF INVENTION:  vectors
;  FILE REFERENCE: 50125/007002
;  CURRENT APPLICATION NUMBER: US/09/714,550
;  CURRENT FILING DATE:  2000-11-16
;  PRIOR APPLICATION NUMBER: US 60/167,439
;  PRIOR FILING DATE: 1999-11-23
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-09-714-550-8

  Query Match             94.6%;  Score 210;  DB 3;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db        552 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 611

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
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Db        612 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 671

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db        672 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 731

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db        732 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 775


RESULT 7
US-08-994-689C-8
; Sequence 8, Application US/08994689C
; Patent No. 6613958
;  GENERAL INFORMATION:
;    APPLICANT:  Neuhold, Lisa
;    APPLICANT:  Killar, Loran
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL MODEL FOR
;    TITLE OF INVENTION:  DEGENERATIVE DISEASES OF CARTILAGE
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/994,689C
;      FILING DATE:  1997-12-19
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Reza
;      REGISTRATION NUMBER:  38,475
;      REFERENCE/DOCKET NUMBER:  0630/0D532
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2792 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-994-689C-8
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  Query Match             94.6%;  Score 210;  DB 3;  Length 2792;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
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Db       2595 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 2654

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db       2655 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 2714

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
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Db       2715 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 2758


RESULT 8
US-09-496-445-4
; Sequence 4, Application US/09496445
; Patent No. 6693226
; GENERAL INFORMATION:
;  APPLICANT: McNeish, John D.
;  APPLICANT: Ahlijnian, Michael K
;  TITLE OF INVENTION: Transgenic Animals Expressing Human p25
;  FILE REFERENCE: PC10142A
;  CURRENT APPLICATION NUMBER: US/09/496,445
;  CURRENT FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 3218
;   TYPE: DNA
;   ORGANISM: Multi organism source
US-09-496-445-4

  Query Match             94.6%;  Score 210;  DB 3;  Length 3218;
  Best Local Similarity   99.1%;  Pred. No. 2.3e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
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Db       2993 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 3052

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
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Db       3053 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 3112

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db       3113 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 3172

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       3173 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3216


RESULT 9
US-08-169-613A-1
; Sequence 1, Application US/08169613A
; Patent No. 6486380
; GENERAL INFORMATION:
;  APPLICANT: Epstein, Paul
;  TITLE OF INVENTION: Pancreatic B Cell Hexokinase Transgene
;  FILE REFERENCE: P0044US0
;  CURRENT APPLICATION NUMBER: US/08/169,613A
;  CURRENT FILING DATE:  1993-12-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3318
;   TYPE: DNA
;   ORGANISM: yeast
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (790)..(2247)
US-08-169-613A-1

  Query Match             94.6%;  Score 210;  DB 3;  Length 3318;
  Best Local Similarity   99.1%;  Pred. No. 2.3e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3037 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 3096

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       3097 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 3156

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
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Db       3157 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 3216

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       3217 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 3260


RESULT 10
US-08-955-565A-6/c
; Sequence 6, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
;  APPLICANT: Malkovsky, Miroslav
;  APPLICANT:  Wells, Andrew
;  TITLE OF INVENTION: Immune Response Enhancer Therapy
;  FILE REFERENCE: WARF-02625
;  CURRENT APPLICATION NUMBER: US/08/955,565A
;  CURRENT FILING DATE:  1997-10-17
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 3740
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-08-955-565A-6

  Query Match             94.6%;  Score 210;  DB 3;  Length 3740;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 1348

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1347 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1288

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 1228

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1227 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1184
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RESULT 11
US-08-675-566-8
; Sequence 8, Application US/08675566
; Patent No. 6090393
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Laurent
;    TITLE OF INVENTION:  PROMOTERS, EXPRESSION CASSETTES,
;    TITLE OF INVENTION:  RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,566
;      FILING DATE:  03-JUL-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2890
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)840-3333
;      TELEFAX:  (212)840-0712
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3822 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-675-566-8

  Query Match             94.6%;  Score 210;  DB 3;  Length 3822;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 961

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        962 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1021

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 1081

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1082 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1125


RESULT 12
US-07-678-408A-1
; Sequence 1, Application US/07678408A
; Patent No. 5266490
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Sam
;    APPLICANT:  Yancopoulos, George D.
;    TITLE OF INVENTION:  Mammalian Expression Vector
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  N.Y.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/678,408A
;      FILING DATE:  19910328
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S.Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  6526-052-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 869-9741
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3944 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
US-07-678-408A-1

  Query Match             94.6%;  Score 210;  DB 2;  Length 3944;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1753 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 1812

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1813 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1872

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1873 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 1932

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1933 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1976


RESULT 13
US-08-675-566-10
; Sequence 10, Application US/08675566
; Patent No. 6090393
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Laurent
;    TITLE OF INVENTION:  PROMOTERS, EXPRESSION CASSETTES,
;    TITLE OF INVENTION:  RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,566
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;       FILING DATE:  03-JUL-1996
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer Esq., William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2890
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)840-3333
;       TELEFAX:  (212)840-0712
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3955 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-675-566-10

  Query Match             94.6%;  Score 210;  DB 3;  Length 3955;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 1094

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1095 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1154

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1155 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 1214

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1215 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1258


RESULT 14
US-08-675-566-9
; Sequence 9, Application US/08675566
; Patent No. 6090393
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Laurent
;    TITLE OF INVENTION:  PROMOTERS, EXPRESSION CASSETTES,
;    TITLE OF INVENTION:  RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,566
;      FILING DATE:  03-JUL-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2890
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)840-3333
;      TELEFAX:  (212)840-0712
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  4009 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-675-566-9

  Query Match             94.6%;  Score 210;  DB 3;  Length 4009;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 1148

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
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Db       1149 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1208

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 1268

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1269 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1312


RESULT 15
US-08-564-313-2/c
; Sequence 2, Application US/08564313
; Patent No. 5910488
;  GENERAL INFORMATION:
;    APPLICANT:  Nabel, Elizabeth
;    APPLICANT:  Nabel, Gary
;    APPLICANT:  Lew, Denise
;    APPLICANT:  Marquet, Magda
;    TITLE OF INVENTION:  PLASMIDS SUITABLE FOR GENE THERAPY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson and Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/564,313
;      FILING DATE:  01-DEC-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/074,344
;      FILING DATE:  07-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  VICAL.033CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4059 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7
US-08-564-313-2

Query Match 94.6%; Score 210; DB 2; Length 4059;
Best Local Similarity 99.1%; Pred. No. 2.4e-46;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1400 ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 1341

Qy         61 AAACATAAAATGAATGCAATTGTTGTTG--AACTTGTTTATTGCAGCTTATAATGGTTAC 118
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1340 AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1281

Qy        119 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1280 AAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGT 1221

Qy        179 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1220 TGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGAT 1177
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Job time : 101.221 secs

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:53:25 ; Search time 1534.75 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	131	91.6	317	3	BP417050	BP417050 BP417050
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c	5	131	91.6	334	7	CV006397	CV006397 CS_gil_12
c	6	131	91.6	353	6	CD279996	CD279996 G43757.10
c	7	131	91.6	362	10	CG478724	CG478724 OST9064 M
c	8	131	91.6	367	10	CG431950	CG431950 Bg140-T3
c	9	131	91.6	369	10	CG431927	CG431927 Bg41-T3 G
c	10	131	91.6	372	1	AL039087	AL039087 DKFZp566H
c	11	131	91.6	373	6	CD280506	CD280506 G43805.34
c	12	131	91.6	380	7	CV161679	CV161679 CS_gil_54
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	15	131	91.6	410	5	BY549695	BY549695 BY549695
	16	131	91.6	413	5	BY563361	BY563361 BY563361
	17	131	91.6	419	5	BY484761	BY484761 BY484761
	18	131	91.6	419	5	BY554859	BY554859 BY554859
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	22	131	91.6	431	5	BY532720	BY532720 BY532720
	23	131	91.6	446	5	BY483187	BY483187 BY483187
	24	131	91.6	448	5	BY571026	BY571026 BY571026
	25	131	91.6	453	5	BY482809	BY482809 BY482809
	26	131	91.6	455	3	BP418262	BP418262 BP418262
	27	131	91.6	461	3	BP418191	BP418191 BP418191
	28	131	91.6	464	5	BY572977	BY572977 BY572977
c	29	131	91.6	464	6	CD280357	CD280357 G43757.71
	30	131	91.6	469	5	BY570855	BY570855 BY570855
c	31	131	91.6	487	7	CV021941	CV021941 CS_gil_20
c	32	131	91.6	490	9	BZ672551	BZ672551 PUBAT69TD
c	33	131	91.6	495	7	CV526695	CV526695 CS_GIL_17
c	34	131	91.6	502	10	CG431922	CG431922 Bg38-T3 G
	35	131	91.6	503	3	BP420735	BP420735 BP420735
	36	131	91.6	507	3	BP420280	BP420280 BP420280
c	37	131	91.6	507	6	CD280879	CD280879 G43756.65
c	38	131	91.6	526	7	CV463249	CV463249 CS_hyp_55
c	39	131	91.6	530	7	CV527488	CV527488 CS_GIL_12
c	40	131	91.6	531	7	CV006382	CV006382 CS_gil_12
c	41	131	91.6	534	7	CV071227	CV071227 CS_gil_39
c	42	131	91.6	536	9	BZ685275	BZ685275 PUBAQ50TD
	43	131	91.6	540	5	BY571556	BY571556 BY571556
c	44	131	91.6	549	6	CD280355	CD280355 G44283.63
c	45	131	91.6	558	6	CD280662	CD280662 G43520.61

ALIGNMENTS

RESULT 1
BZ666890/c
LOCUS BZ666890 264 bp DNA linear GSS 05-FEB-2003
DEFINITION PUBFP64TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa044K08, genomic survey sequence.
ACCESSION BZ666890
VERSION BZ666890.1 GI:28212735
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 264)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .264
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa044K08"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high CoT selected genomic DNA library"
ORIGIN

Query Match 91.6%; Score 131; DB 9; Length 264;
Best Local Similarity 98.6%; Pred. No. 3.3e-25;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58

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Db        222 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 163

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 103

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        102 CAAGTAAAACCTCTACAAATGTGGT 78


RESULT 2
CD282637/c
LOCUS       CD282637                 278 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G38935.14 NCI_CGAP_ZEmb2 Danio rerio cDNA clone IMAGE:6519507 5',
            mRNA sequence.
ACCESSION   CD282637
VERSION     CD282637.1  GI:31060413
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 278)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 14103  row: L  column: 3
            High quality sequence stop: 278.
FEATURES             Location/Qualifiers
     source          1. .278
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6519507"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb2"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            91.6%;  Score 131;  DB 6;  Length 278;
  Best Local Similarity  98.6%;  Pred. No. 3.3e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        178 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 119

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 59

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         58 CAAGTAAAACCTCTACAAATGTGGT 34


RESULT 3
BP417050
LOCUS       BP417050                 317 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP417050 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE00046r 3', mRNA sequence.
ACCESSION   BP417050
VERSION     BP417050.1  GI:66783299
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .317
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE00046r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match            91.6%;  Score 131;  DB 3;  Length 317;
  Best Local Similarity  98.6%;  Pred. No. 3.3e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        148 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 207

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 267

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        268 CAAGTAAAACCTCTACAAATGTGGT 292


RESULT 4
CG431929/c
LOCUS       CG431929                 331 bp    DNA     linear   GSS 16-SEP-2003
DEFINITION  Bg32-T3 Glomus intraradices Bgl II library (in pBK-CMV stratagene)
            Glomus intraradices genomic clone Bg32-T3, genomic survey sequence.
ACCESSION   CG431929
VERSION     CG431929.1  GI:34766795
KEYWORDS    GSS.
SOURCE      Glomus intraradices
  ORGANISM  Glomus intraradices
            Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
            Glomeraceae; Glomus.
REFERENCE   1  (bases 1 to 331)
  AUTHORS   Lammers,P.J., Ratyanaka,S., Rehrer,C. and Jun,J.
  TITLE     Genomic sequence from Glomus intraradices spore tissue
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Peter Lammers
            New Mexico State University
            BOX 30001, 3MLS, Las Cruces, NM 88003, USA
            Tel: 505-646-3918
            Fax: 505-646-6846
```

```
            Email: plammers@nmsu.edu
            Result of blastx search of NCBI non-redundant protein database,
            June 2003: Highest scoring result, with an E-value of 2e-06 was
            gi|224398|prf||1103278B ORF
            Seq primer: T3
            Class: plasmid ends
            High quality sequence stop: 331.
FEATURES              Location/Qualifiers
     source           1. .331
                      /organism="Glomus intraradices"
                      /mol_type="genomic DNA"
                      /strain="DAOM 197198, Biosystematic Research Center,
                      Ottawa"
                      /db_xref="taxon:4876"
                      /clone="Bg32-T3"
                      /tissue_type="Spores"
                      /lab_host="E. coli XLR Blue"
                      /clone_lib="Glomus intraradices Bgl II library (in pBK-CMV
                      stratagene)"
                      /note="Vector: pBK-CMV; genomic DNA isolated from Spores;
                      complete Bgl II digest of gDNA; cloned into BamHI site of
                      pBK-CMV"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 10;  Length 331;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        165 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 106

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 46

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         45 CAAGTAAAACCTCTACAAATGTGGT 21


RESULT 5
CV006397/c
LOCUS       CV006397                334 bp    mRNA    linear   EST 18-AUG-2004
DEFINITION  CS_gil_12H12_M13Reverse Blue crab gill, normalized Callinectes
            sapidus cDNA clone CS_gil_12H12 5' similar to prf|1103278B ORF.
            Score = 89.0 bits (219), Expect = 3e-17, mRNA sequence.
ACCESSION   CV006397
VERSION     CV006397.1  GI:51365620
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 12  row: H  column: 12
            Seq primer: M13 Reverse
            High quality sequence stop: 324.
FEATURES              Location/Qualifiers
     source           1. .334
                      /organism="Callinectes sapidus"
                      /mol_type="mRNA"
                      /db_xref="taxon:6763"
                      /clone="CS_gil_12H12"
                      /tissue_type="Pooled anterior and posterior gills from
                      crabs acclimated to salinities of 35 and 5 parts per
                      thousand"
                      /dev_stage="Adult intermolt"
                      /clone_lib="Blue crab gill, normalized"
                      /note="Vector: pCMV Sport 6.1; Total RNA samples were
                      prepared individually from each tissue, checked for
                      quality, and then pooled for construction and
                      normalization of a cDNA library by Invitrogen.  Plasmids
                      were isolated and inserts sequenced from their 5'-ends by
                      the Blue Crab Molecular Genetics Laboratory at the
                      University of North Carolina Wilmington.  Traces were
                      trimmed, compared (BLASTx) to NCBI non-redundant protein
                      database as of 19 July 2004, and processed for submission
                      to dbEST by trace2dbEST software (Parkinson, Anthony and
                      Blaxter, unpublished software)."
ORIGIN

  Query Match             91.6%;  Score 131;  DB 7;  Length 334;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        223 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 164

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 104

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        103 CAAGTAAAACCTCTACAAATGTGGT 79


RESULT 6
CD279996/c
LOCUS       CD279996                353 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43757.10 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6321722 5',
            mRNA sequence.
ACCESSION   CD279996
VERSION     CD279996.1  GI:31057772
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 353)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13762  row: C  column: 3
            High quality sequence stop: 353.
FEATURES              Location/Qualifiers
     source           1. .353
                      /organism="Danio rerio"
                      /mol_type="mRNA"
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                     /db_xref="taxon:7955"
                     /clone="IMAGE:6321722"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 353;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        226 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 167

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 107

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        106 CAAGTAAAACCTCTACAAATGTGGT 82


RESULT 7
CG478724/c
LOCUS       CG478724                 362 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST9064 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST9064, mRNA
            sequence.
ACCESSION   CG478724
VERSION     CG478724.1  GI:37229613
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
   PUBMED   14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .362
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST9064"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 10;  Length 362;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        324 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 265

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 205

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        204 CAAGTAAAACCTCTACAAATGTGGT 180


RESULT 8
CG431950/c
LOCUS       CG431950                 367 bp    DNA     linear   GSS 16-SEP-2003
DEFINITION  Bg140-T3 Glomus intraradices Bgl II library (in pBK-CMV stratagene)
            Glomus intraradices genomic clone Bg140-T3, genomic survey
            sequence.
ACCESSION   CG431950
VERSION     CG431950.1  GI:34766816
KEYWORDS    GSS.
SOURCE      Glomus intraradices
  ORGANISM  Glomus intraradices
            Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
            Glomeraceae; Glomus.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Lammers,P.J., Ratyanaka,S., Rehrer,C. and Jun,J.
  TITLE     Genomic sequence from Glomus intraradices spore tissue
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Peter Lammers
            New Mexico State University
            BOX 30001, 3MLS, Las Cruces, NM 88003, USA
            Tel: 505-646-3918
            Fax: 505-646-6846
            Email: plammers@nmsu.edu
            Result of blastx search of NCBI non-redundant protein database,
            June 2003: Highest scoring result, with an E-value of 1e-06 was
            gi|224398|prf||1103278B ORF
            Seq primer: T3
            Class: plasmid ends
            High quality sequence stop: 367.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Glomus intraradices"
                     /mol_type="genomic DNA"
                     /strain="DAOM 197198, Biosystematic Research Center,
                     Ottawa"
                     /db_xref="taxon:4876"
                     /clone="Bg140-T3"
                     /tissue_type="Spores"
                     /lab_host="E. coli XLR Blue"
                     /clone_lib="Glomus intraradices Bgl II library (in pBK-CMV
                     stratagene)"
                     /note="Vector: pBK-CMV; genomic DNA isolated from Spores;
                     complete Bgl II digest of gDNA; cloned into BamHI site of
                     pBK-CMV"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 10;  Length 367;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        164 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 105

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        104 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 45

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         44 CAAGTAAAACCTCTACAAATGTGGT 20


RESULT 9
CG431927/c
LOCUS       CG431927                369 bp    DNA     linear   GSS 16-SEP-2003
DEFINITION  Bg41-T3 Glomus intraradices Bgl II library (in pBK-CMV stratagene)
            Glomus intraradices genomic clone Bg41-T3, genomic survey sequence.
ACCESSION   CG431927
VERSION     CG431927.1  GI:34766793
KEYWORDS    GSS.
SOURCE      Glomus intraradices
  ORGANISM  Glomus intraradices
            Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
            Glomeraceae; Glomus.
REFERENCE   1  (bases 1 to 369)
  AUTHORS   Lammers,P.J., Ratyanaka,S., Rehrer,C. and Jun,J.
  TITLE     Genomic sequence from Glomus intraradices spore tissue
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Peter Lammers
            New Mexico State University
            BOX 30001, 3MLS, Las Cruces, NM 88003, USA
            Tel: 505-646-3918
            Fax: 505-646-6846
            Email: plammers@nmsu.edu
            Result of blastx search of NCBI non-redundant protein database,
            June 2003: Highest scoring result, with an E-value of 1e-06 was
            gi|224398|prf||1103278B ORF
            Seq primer: T3
            Class: plasmid ends
            High quality sequence stop: 369.
FEATURES             Location/Qualifiers
     source          1. .369
                     /organism="Glomus intraradices"
                     /mol_type="genomic DNA"
                     /strain="DAOM 197198, Biosystematic Research Center,
                     Ottawa"
                     /db_xref="taxon:4876"
                     /clone="Bg41-T3"
                     /tissue_type="Spores"
                     /lab_host="E. coli XLR Blue"
                     /clone_lib="Glomus intraradices Bgl II library (in pBK-CMV
                     stratagene)"
                     /note="Vector: pBK-CMV; genomic DNA isolated from Spores;
                     complete Bgl II digest of gDNA; cloned into BamHI site of
                     pBK-CMV"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 10;  Length 369;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        165 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 106

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 46

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         45 CAAGTAAAACCTCTACAAATGTGGT 21


RESULT 10
AL039087/c
LOCUS       AL039087                372 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566H204_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566H204 3', mRNA sequence.
ACCESSION   AL039087
VERSION     AL039087.1  GI:5408188
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Bloecker, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 3' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No r1 sequence available.
            This clone (DKFZp566H204) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566H204"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 1;  Length 372;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        278 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 219

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 159

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        158 CAAGTAAAACCTCTACAAATGTGGT 134


RESULT 11
CD280506/c
LOCUS       CD280506                373 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43805.34 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6322113 5',
            mRNA sequence.
ACCESSION   CD280506
VERSION     CD280506.1  GI:31058282
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
```

```
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13763  row: C  column: 10
            High quality sequence stop: 373.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6322113"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 373;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        299 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAGCAA 240

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 180

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        179 CAAGTAAAACCTCTACAAATGTGGT 155


RESULT 12
CV161679/c
LOCUS       CV161679                380 bp    mRNA    linear   EST 08-SEP-2004
DEFINITION  CS_gil_54H02_M13Reverse Blue crab gill, normalized Callinectes
            sapidus cDNA clone CS_gil_54H02 5' similar to prf|1103278B ORF.
            Score = 60.8 bits (146), Expect = 9e-09, mRNA sequence.
ACCESSION   CV161679
VERSION     CV161679.1  GI:51946943
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 54  row: H  column: 02
            Seq primer: M13 Reverse
            High quality sequence stop: 350.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_gil_54H02"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match             91.6%;  Score 131;  DB 7;  Length 380;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        175 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 116

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 56

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         55 CAAGTAAAACCTCTACAAATGTGGT 31


RESULT 13
CD280768/c
LOCUS       CD280768                390 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43520.87 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6322364 5',
            mRNA sequence.
ACCESSION   CD280768
VERSION     CD280768.1  GI:31058544
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 390)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
```

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           Plate: 13763  row: M  column: 21
           High quality sequence stop: 390.
FEATURES             Location/Qualifiers
     source          1. .390
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6322364"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 390;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        309 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 250

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 190

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        189 CAAGTAAAACCTCTACAAATGTGGT 165


RESULT 14
BP420484
LOCUS       BP420484                395 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420484 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE03774r 3', mRNA sequence.
ACCESSION   BP420484
VERSION     BP420484.1  GI:66786737
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE03774r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 3;  Length 395;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        123 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 182

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 242

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        243 CAAGTAAAACCTCTACAAATGTGGT 267


RESULT 15
BY549695
LOCUS       BY549695                410 bp    mRNA    linear   EST 14-DEC-2002
DEFINITION  BY549695 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730210L20 3', mRNA sequence.
ACCESSION   BY549695
VERSION     BY549695.1  GI:26884074
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
```

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730210L20"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 5;  Length 410;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-25;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        266 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 325

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 385

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        386 CAAGTAAAACCTCTACAAATGTGGT 410
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Search completed: November 22, 2005, 01:21:29
Job time : 1536.75 secs

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:49:24 ; Search time 216.327 Seconds
(without alignments)
4405.602 Million cell updates/sec

Title: US-10-683-775-1_COPY_80_222
Perfect score: 143
Sequence: 1 aatttgtgatgctattgctt.....aaaacctctacaaatgtggt 143

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	143	100.0	222	5	AAF30815	Aaf30815 SV40 late
c	2	143	100.0	222	5	AAF30816	Aaf30816 SV40 earl
	3	131	91.6	222	12	ADL26564	Adl26564 SV40 late
c	4	131	91.6	230	4	AAH27520	Aah27520 SV40 tran
c	5	131	91.6	239	4	AAF82390	Aaf82390 SV40 geno
	6	131	91.6	250	8	ADA50602	Ada50602 SV40 poly
	7	131	91.6	275	14	AEB72706	Aeb72706 SV40 poly
	8	131	91.6	285	8	ACC69400	Acc69400 SV40 poly
	9	131	91.6	285	8	AAD48560	Aad48560 SV40 poly
	10	131	91.6	285	9	ACC69365	Acc69365 SV40 poly
	11	131	91.6	285	13	ADV70462	Adv70462 SV40 poly
	12	131	91.6	296	2	AAV35371	Aav35371 Human INO
	13	131	91.6	296	2	AAZ32097	Aaz32097 pGL3 basi
	14	131	91.6	452	13	ADW93253	Adw93253 SV40 DNA
c	15	131	91.6	481	14	ADY84551	Ady84551 SV40 poly
	16	131	91.6	509	14	ADZ66620	Adz66620 Simian vi
c	17	131	91.6	532	14	AEA48004	Aea48004 Lentivira
	18	131	91.6	667	5	AAD04943	Aad04943 Insert se
	19	131	91.6	677	2	AAT97157	Aat97157 SV40 poly
c	20	131	91.6	717	3	AAA74636	Aaa74636 Plasmid p
	21	131	91.6	770	5	AAD04942	Aad04942 Insert se
c	22	131	91.6	782	5	AAH20736	Aah20736 SV40 DNA
c	23	131	91.6	816	14	ADV21047	Adv21047 4x-Polyad
c	24	131	91.6	816	14	ADY66741	Ady66741 4X-polyad
	25	131	91.6	828	1	AAN81632	Aan81632 SV40 init
	26	131	91.6	1193	6	AAL42929	Aal42929 Medaka ov
	27	131	91.6	1223	4	AAL02861	Aal02861 Human rep
	28	131	91.6	1359	4	AAS41785	Aas41785 Genomic s
	29	131	91.6	1359	4	AAS41797	Aas41797 Genomic s
	30	131	91.6	1359	4	AAS41878	Aas41878 Genomic s
	31	131	91.6	1359	4	AAS41845	Aas41845 Genomic s
	32	131	91.6	1359	4	AAS41831	Aas41831 Genomic s
	33	131	91.6	1359	4	AAS41894	Aas41894 Genomic s
	34	131	91.6	1359	4	AAK85458	Aak85458 Human imm
	35	131	91.6	1359	4	AAK85525	Aak85525 Human imm
	36	131	91.6	1359	4	AAK85475	Aak85475 Human imm
	37	131	91.6	1359	4	AAK69632	Aak69632 Human imm
	38	131	91.6	1359	4	AAK85508	Aak85508 Human imm
	39	131	91.6	1359	4	AAK69645	Aak69645 Human imm
	40	131	91.6	1359	4	AAL02859	Aal02859 Human rep
	41	131	91.6	1359	4	AAL02903	Aal02903 Human rep
	42	131	91.6	1359	4	AAL02870	Aal02870 Human rep
	43	131	91.6	1362	4	AAS41789	Aas41789 Genomic s
	44	131	91.6	1362	4	AAS41882	Aas41882 Genomic s
	45	131	91.6	1362	4	AAS41833	Aas41833 Genomic s

ALIGNMENTS

RESULT 1
AAF30815
ID AAF30815 standard; DNA; 222 BP.
XX
AC AAF30815;
XX
DT 21-JUN-2001 (first entry)
XX
DE SV40 late polyadenylation site.
XX
KW SV40; polyadenylation; vector; ss.
XX
OS Rhesus macaque polyoma virus.
XX
FH Key Location/Qualifiers
FT polyA_signal 123. .128
FT /*tag= a
FT misc_feature 151. .187
FT /*tag= b
FT /note= "G/T rich region"
XX
PN WO200127299-A1. ✓
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028431.
XX
PR 13-OCT-1999; 99US-0159177P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Mcgrew JT;
XX
DR WPI; 2001-290726/30.
XX
PT An expression vector for increasing the yield of recombinant protein
PT comprises a first protein operably linked to a second protein.
XX
PS Claim 4; Page 28; 41pp; English.
XX
CC The present sequence is that of the SV40 late polyadenylation site. This
CC SV40 late polyadenylation site, or nucleotides 80-222 of it, is utilised

CC in a claimed expression vector. The vector comprises a promoter sequence,
CC a first coding sequence, a polyadenylation site (preferably SV40 late or
CC early polyadenylation site), and a second coding sequence, preferably
CC encoding a selectable marker such as dihydrofolate reductase. The
CC internal polyadenylation site allows a single promoter to generate both
CC monocistronic messages and dicistronic messages. An internal ribosome
CC entry site (IRES) may be inserted between the internal polyadenylation
CC site and the DNA encoding the selectable marker. Similar, multicistronic
CC vectors can also be prepared. Cells transfected with the vector, and cell
CC lines cloned from them, are also claimed. These are used for obtaining a
CC recombinant protein in mammalian host cells. The expression vector is
CC useful as it comprises a selectable, amplifiable marker, while increasing
CC the proportion of mRNAs encoding a desired recombinant protein
XX
SQ Sequence 222 BP; 76 A; 30 C; 45 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 143; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.4e-30;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 139

Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 199

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||
Db        200 AGTAAAACCTCTACAAATGTGGT 222
```

RESULT 2
AAF30816/c
ID AAF30816 standard; DNA; 222 BP.
XX
AC AAF30816;
XX
DT 21-JUN-2001 (first entry)
XX
DE SV40 early polyadenylation site.
XX
KW SV40; polyadenylation; vector; ss.
XX
OS Rhesus macaque polyoma virus.
XX
PN WO200127299-A1.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028431.
XX
PR 13-OCT-1999; 99US-0159177P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Mcgrew JT;
XX
DR WPI; 2001-290726/30.
XX
PT An expression vector for increasing the yield of recombinant protein
PT comprises a first protein operably linked to a second protein.
XX
PS Claim 4; Page 28-29; 41pp; English.
XX
CC The present sequence is that of the SV40 early polyadenylation site. This
CC SV40 early polyadenylation site can be utilised in a claimed expression
CC vector. The vector comprises a promoter sequence, a first coding
CC sequence, a polyadenylation site (preferably SV40 late or early
CC polyadenylation site), and a second coding sequence, preferably encoding
CC a selectable marker such as dihydrofolate reductase. The internal
CC polyadenylation site allows a single promoter to generate both
CC monocistronic messages and dicistronic messages. An internal ribosome
CC entry site (IRES) may be inserted between the internal polyadenylation
CC site and the DNA encoding the selectable marker. Similar, multicistronic
CC vectors can also be prepared. Cells transfected with the vector, and cell
CC lines cloned from them, are also claimed. These are used for obtaining a
CC recombinant protein in mammalian host cells. The expression vector is
CC useful as it comprises a selectable, amplifiable marker, while increasing
CC the proportion of mRNAs encoding a desired recombinant protein
XX
SQ Sequence 222 BP; 71 A; 45 C; 30 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 143; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.4e-30;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 84

Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 24

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||
Db         23 AGTAAAACCTCTACAAATGTGGT 1
```

RESULT 3
ADL26564
ID ADL26564 standard; DNA; 222 BP.
XX
AC ADL26564;
XX
DT 03-JUN-2004 (first entry)
XX
DE SV40 late polyA signal sequence.
XX
KW cytostatic; gene therapy; vaccine; cancer; immune response; ds;
KW late polyA signal sequence; SV40.
XX
OS Simian virus 40.
XX
PN WO2004019886-A2.
XX
PD 11-MAR-2004.
XX
PF 29-AUG-2003; 2003WO-US027125.
XX
PR 29-AUG-2002; 2002US-0407492P.
XX
PA (CYTO-) CYTOCURE LLC.
XX
PI Durda PJ, Kurnick JT, Dunn IS;
XX
DR WPI; 2004-239114/22.
XX
PT Increasing an immune response against a tumor cell comprises
PT administering to a subject with a tumor an amount of IFN-beta receptor
PT agonist and tumor associated antigen (TAA).
XX
PS Example 6; Page 44; 80pp; English.
XX
CC The present invention relates to a method of increasing an immune
CC response against a tumour cell, comprising administering to a subject
CC with a tumour an amount of IFN-beta receptor agonist and tumour
CC associated antigen (TAA). The method is useful for increasing an immune
CC response against a tumour cell. The present sequence is the polyA signal
CC sequence from SV40 which was used in the exemplification of the
CC invention.
XX
SQ Sequence 222 BP; 78 A; 29 C; 45 G; 70 T; 0 U; 0 Other;

```
  Query Match             91.6%;  Score 131;  DB 12;  Length 222;
  Best Local Similarity   98.6%;  Pred. No. 7.5e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db         77 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 136

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 196

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        197 CAAGTAAAACCTCTACAAATGTGGT 221


RESULT 4
AAH27520/c
ID   AAH27520 standard; DNA; 230 BP.
XX
AC   AAH27520;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SV40 transcriptional terminator.
XX
KW   SV40; transcriptional terminator; pesticide; antisense therapy;
KW   pest control; gene expression inhibition; baculovirus transfer plasmid;
KW   dsRNA expression; ds.
XX
OS   Rhesus macaque polyoma virus.
XX
PN   WO200134815-A1.
XX
PD   17-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030367.
XX
PR   05-NOV-1999;   99US-0164078P.
PR   24-NOV-1999;   99US-00448256.
XX
PA   (CAMB-) CAMBRIA BIOSCIENCES LLC.
XX
PI   Liu L,  Chouinard S,  Velema J;
XX
DR   WPI; 2001-329087/34.
XX
PT   Pest control agent comprises an expression vector which expresses sense
PT   and antisense RNA directed to pest genes.
XX
PS   Example 1; Fig 7; 72pp; English.
XX
CC   The invention relates to a pest control agent comprising at least one
CC   expression vector which directs transcription of at least one RNA that,
CC   when present in a cell, forms a double-stranded structure that inhibits
CC   expression of at least one gene in the cell. The agents and method are
CC   useful for controlling pests and inhibiting the expression of a gene in
CC   an insect cell. Viral replication is not needed for the pesticide to
CC   work. The present sequence is the SV40 transcriptional terminator, which
CC   was incorporated into a baculovirus transfer plasmid used for expression
CC   of dsRNA in an exemplification of the invention
XX
SQ   Sequence 230 BP; 76 A; 47 C; 29 G; 78 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 4;  Length 230;
  Best Local Similarity   98.6%;  Pred. No. 7.5e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        162 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 103

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 43

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         42 CAAGTAAAACCTCTACAAATGTGGT 18


RESULT 5
AAF82390/c
ID   AAF82390 standard; DNA; 239 BP.
XX
AC   AAF82390;
XX
DT   25-JUN-2001  (first entry)
XX
DE   SV40 genome poly(A) site.
XX
KW   Simian virus 40; chicken embryo lethal orphan virus; CELO; vaccine;
KW   recombinant avian egg; chicken adenovirus expression vector; AdCEV;
KW   recombinant protein production; vector; gene therapy; ds.
XX
OS   Rhesus macaque polyoma virus.
XX
PN   WO200119968-A1.
XX
PD   22-MAR-2001.
XX
PF   15-SEP-2000; 2000WO-US025489.
XX
PR   17-SEP-1999;   99US-0154393P.
XX
PA   (CHEM-) CHEMOGEN INC.
XX
PI   Grabko VI,  Blyden ER;
XX
DR   WPI; 2001-328015/34.
XX
PT   Use of avian adenovirus for producing recombinant proteins by mixing
PT   vector containing avian adenovirus DNA with purified adenovirus DNA,
PT   introducing DNA mixture into embryonated avian egg, and harvesting
PT   proteins.
XX
PS   Example 3; Page 52; 70pp; English.
XX
CC   The present sequence is the poly(A) site of the simian virus 40 genome.
CC   The sequence was used in an example illustrating an invention relating to
CC   the use of avian adenovirus for producing recombinant proteins in an
CC   avian egg. The method involves preparing a vector containing avian
CC   adenovirus DNA, preparing a mixture of vector DNA with purified
CC   adenovirus DNA or adenovirus particles, introducing mixture into
CC   embryonated avian egg or avian cell culture, incubating, and harvesting
CC   fluids from egg containing recombinant protein molecule encoded by vector
CC   DNA. The method is useful for producing recombinant proteins such as
CC   therapeutic proteins, immunostimulatory proteins, or tumour antigens in
CC   an avian egg. The eggs may be used as a vaccine to elicit an
CC   immunological response to the antigenic portion of the protein encoded by
CC   the DNA present in the chimeric gene of a prepared infectious adenovirus.
CC   The chicken adenovirus expression vector (AdCEV)/egg system is simple and
CC   economical and allows isolation of the protein in a biologically active
CC   form, free of endotoxins
XX
SQ   Sequence 239 BP; 76 A; 50 C; 32 G; 81 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 4;  Length 239;
  Best Local Similarity   98.6%;  Pred. No. 7.6e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        161 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 102
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```
Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 42

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db         41 CAAGTAAAACCTCTACAAATGTGGT 17
```

RESULT 6
ADA50602
ID ADA50602 standard; DNA; 250 BP.
XX
AC ADA50602;
XX
DT 20-NOV-2003 (first entry)
XX
DE SV40 polyadenylation signal (late and early), SEQ ID NO:57.
XX
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
KW humoral response; cellular response; immune response; immunotherapy;
KW cancer; cytostatic; vaccine; gene therapy; SV40; ds.
XX
OS Simian virus 40.
XX
PN WO2003031569-A2.
XX
PD 17-APR-2003.
XX
PF 18-SEP-2002; 2002WO-US029640.
XX
PR 10-OCT-2001; 2001US-0328371P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;
PI Branigan PJ;
XX
DR WPI; 2003-393437/37.
XX
PT New nucleic acid vaccine, useful for eliciting an immune response to a
PT cancer associated tumor protein in a mammal.
XX
PS Disclosure; Page 50; 92pp; English.
XX
CC The invention relates to a nucleic acid vaccine comprising one or more
CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,
CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
CC is preferably under the control of a promoter such as the cytomegalovirus
CC immediate early promoter, the dihydrofoliate reductase promoter or the
CC early or late SV40 promoters. The invention also encompasses the method
CC of eliciting an immune response to a tumour antigen in a mammal using the
CC vaccine of the invention. Coexpression of the antigen and adjuvant
CC induces a humoral or cellular response to the tumour antigen, generating
CC an immune reponse useful for treatment or prophylaxis of cancers. The
CC present sequence represents a regulatory nucleic acid used in DNA vaccine
CC vectors of the invention.
XX
SQ Sequence 250 BP; 85 A; 33 C; 54 G; 78 T; 0 U; 0 Other;

```
  Query Match             91.6%;  Score 131;  DB 8;  Length 250;
  Best Local Similarity   98.6%;  Pred. No. 7.7e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db         84 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 143

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 203

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        204 CAAGTAAAACCTCTACAAATGTGGT 228
```

RESULT 7
AEB72706
ID AEB72706 standard; DNA; 275 BP.
XX
AC AEB72706;
XX
DT 20-OCT-2005 (first entry)
XX
DE SV40 polyadenylation signal.
XX
KW Plasmid; vector; gene expression; polyadenylation signal; ds.
XX
OS Simian virus 40.
XX
PN US2005175591-A1.
XX
PD 11-AUG-2005.
XX
PF 28-JAN-2005; 2005US-00046219.
XX
PR 28-JAN-2004; 2004US-0539857P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Stout JT, Mcfarland T, Francis PJ, Appukuttan B;
XX
DR WPI; 2005-541742/55.
XX
PT Novel DNA molecule comprising human soluble neuropilin-1 polyadenylation
PT signal, useful for expressing polypeptide in cell, in genetic engineering
PT and for constructing viral vectors.
XX
PS Disclosure; Fig 2; 25pp; English.
XX
CC The invention relates to isolated DNA molecules, especially expression
CC constructs, comprising the 17 bp polyadenylation signal from the human
CC soluble neuropilin-1 (sNRP) gene (AEB72704). This polyadenylation signal
CC is situated downstream of the GT splice donor site of intron 12 of the
CC full-length neuropilin-1 gene, and also functions as the termination
CC codon for sNRP. It efficiently facilitates addition of poly(A) tails to
CC RNAs expressed in cells and has similar activity to the 276 bp SV40
CC polyadenylation signal that is currently used in expression vectors. Use
CC of this shorter dual termination/polyadenylation signal avoids the need
CC for large and cumbersome polyadenylation signals, permitting expression
CC vectors to be engineered to carry considerably larger genes than has
CC previously been possible. The sNRP termination/polyadenylation signal may
CC be used in constructs, including plasmid or viral vectors, for the
CC expression of a variety of genes. Such genes include reporter genes
CC (especially humanized red shifted green fluorescent protein (hrGFP), beta
CC -galactosidase and luciferase) or therapeutic genes such as Bik, Bad,
CC Bak, Bax, Bcl-XL, Gax, X-linked inhibitor of apoptosis protein (XIAP),
CC cellular inhibitor of apoptosis protein (cIAP)-1, cIAP-2, p16, p21, p27,
CC p53, retinoblastoma gene (pRb), the constitutively active form of pRb,
CC PTEN, tissue inhibitor of metalloproteinase (TIMP)-1, TIMP-2, TIMP-3,
CC TIMP-4, endostatin, angiostatin, endostatin XVIII, endostatin XV, the C-
CC terminal hemopexin domain of matrix metalloproteinase-2, the kringle 5
CC domain of human plasminogen, a fusion protein of endostatin and
CC angiostatin, a fusion protein of endostatin and angiostatin, a fusion
CC protein of endostatin and the kringle 5 domain of human plasminogen, the
CC monokine-induced by interferon-gamma (Mig), the interferon-alpha
CC inducible protein 10 (IP-10), a fusion protein of Mig and IP-10, soluble
CC FLT-1 (fms-like tyrosine kinase 1 receptor), and kinase insert domain
CC receptor (KDR). The present sequence represents 275 bp of the SV40
CC polyadenylation signal.
XX

```
SQ   Sequence 275 BP; 91 A; 34 C; 55 G; 95 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 14;  Length 275;
  Best Local Similarity   98.6%;  Pred. No. 7.8e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        112 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 171

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 231

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        232 CAAGTAAAACCTCTACAAATGTGGT 256


RESULT 8
ACC69400
ID   ACC69400 standard; DNA; 285 BP.
XX
AC   ACC69400;
XX
DT   15-JUL-2003  (first entry)
XX
DE   SV40 polyadenylation signal sequence SEQ ID NO:8.
XX
KW   Transgenic avian; chicken; cytoplasmic injection; genetic analysis;
KW   genetic mechanism; genetic function; lysozyme; interferon alpha 2b; gene;
KW   ds.
XX
OS   Rhesus macaque polyoma virus.
XX
PN   WO2003025146-A2.
XX
PD   27-MAR-2003.
XX
PF   18-SEP-2002; 2002WO-US029878.
XX
PR   18-SEP-2001; 2001US-0322969P.
PR   25-JAN-2002; 2002US-0351550P.
XX
PA   (AVIG-) AVIGENICS INC.
XX
PI   Rapp JC,  Christmann L;
XX
DR   WPI; 2003-363141/34.
XX
PT   Producing a transgenic avian, e.g. chicken, useful as a model for various
PT   diseases in humans and other animals, comprises introducing a nucleic
PT   acid encoding a heterologous protein into the avian embryo by cytoplasmic
PT   injection.
XX
PS   Disclosure; Fig 4; 192pp; English.
XX
CC   The present invention describes a method for producing a transgenic
CC   avian. The method comprises microinjecting into a cell of an avian embryo
CC   a nucleic acid comprising a transgene having a nucleotide sequence
CC   encoding a heterologous polypeptide; introducing the microinjected avian
CC   embryo into an oviduct of a recipient hen, such that the recipient hen
CC   lays a shelled egg containing the microinjected avian embryo; and
CC   incubating the shelled egg containing the microinjected avian embryo
CC   until the shelled egg hatches, and so producing a transgenic avian
CC   containing the transgene. Also described: (1) a transgenic avian produced
CC   by the above method and that produces at least one heterologous
CC   polypeptide in egg white, where the transgenic avian or founder ancestor
CC   of the transgenic avian was not produced using a eukaryotic viral vector;
CC   (2) an avian egg produced by the transgenic avian cited above; and (3) a
CC   heterologous protein produced by the transgenic avian, comprising a
CC   heterologous polypeptide selected from a cytokine, a hormone, an enzyme,
CC   a structural protein, and an immunoglobulin polypeptide. The method is
CC   useful in producing a transgenic avian, particularly chicken, by
CC   cytoplasmic injection. The transgenic animal can be used as models for
CC   various diseases in humans and other animals and for studying genetics
CC   and understanding genetic mechanisms and functions. The present sequence
CC   represents the SV40 polyadenylation signal sequence, which is given in
CC   the exemplification of the present invention
XX
SQ   Sequence 285 BP; 92 A; 46 C; 68 G; 79 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 8;  Length 285;
  Best Local Similarity   98.6%;  Pred. No. 7.9e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        111 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 170

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 230

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        231 CAAGTAAAACCTCTACAAATGTGGT 255


RESULT 9
AAD48560
ID   AAD48560 standard; DNA; 285 BP.
XX
AC   AAD48560;
XX
DT   24-FEB-2003  (first entry)
XX
DE   SV40 polyadenylation signal sequence.
XX
KW   Lysozyme gene expression control region; chromosomal positional effect;
KW   transgene; avian cell; SV40; ds.
XX
OS   Rhesus macaque polyoma virus.
XX
PN   WO200279447-A2.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US009866.
XX
PR   30-MAR-2001; 2001US-0280004P.
PR   03-AUG-2001; 2001US-00922549.
PR   25-JAN-2002; 2002US-0351550P.
XX
PA   (AVIG-) AVIGENICS INC.
XX
PI   Rapp JC;
XX
DR   WPI; 2003-046807/04.
XX
PT   New isolated or recombinant nucleic acid for reducing the chromosomal
PT   positional effect of a transgene, comprises an isolated avian lysozyme
PT   gene expression control region.
XX
PS   Claim 10; Fig 6; 88pp; English.
XX
CC   The invention relates to an isolated or recombinant nucleic acid or DNA
CC   molecule comprising an isolated avian lysozyme gene expression control
CC   region operably linked to a nucleic acid insert encoding a polypeptide.
CC   The nucleic acid is useful for reducing the chromosomal positional effect
CC   of a transgene operably linked to the lysozyme gene expression control
CC   region and transfected into a recipient avian cell. The present sequence
CC   is SV40 polyadenylation signal sequence
XX
SQ   Sequence 285 BP; 92 A; 46 C; 68 G; 79 T; 0 U; 0 Other;
```

```
  Query Match             91.6%;  Score 131;  DB 8;  Length 285;
  Best Local Similarity   98.6%;  Pred. No. 7.9e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        111 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 170

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 230

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        231 CAAGTAAAACCTCTACAAATGTGGT 255


RESULT 10
ACC69365
ID   ACC69365 standard; DNA; 285 BP.
XX
AC   ACC69365;
XX
DT   15-JUL-2003  (first entry)
XX
DE   SV40 polyadenylation signal sequence SEQ ID NO:8.
XX
KW   Transgenic avian; sperm-mediated transfection; pharmaceutical;
KW   diagnostic; livestock feed additive; gene; ds.
XX
OS   Rhesus macaque polyoma virus.
XX
PN   WO2003024199-A2.
XX
PD   27-MAR-2003.
XX
PF   23-SEP-2002; 2002WO-US030156.
XX
PR   21-SEP-2001; 2001US-0323961P.
PR   21-SEP-2001; 2001US-0324001P.
XX
PA   (AVIG-) AVIGENICS INC.
XX
PI   Rapp JC,  Sutrave P;
XX
DR   WPI; 2003-363068/34.
XX
PT   Generating a transgenic avian zygote by sperm-mediated transfection, for
PT   producing heterologous proteins, comprise introducing to avian male germ
PT   cells a nucleic acid comprising a transgene encoding heterologous
PT   polypeptide.
XX
PS   Disclosure; Fig 4; 167pp; English.
XX
CC   The present invention describes a method for generating a transgenic
CC   avian zygote by sperm-mediated transfection which comprises introducing a
CC   nucleic acid comprising a transgene having a nucleotide sequence encoding
CC   a heterologous polypeptide to the avian male germ cells by lipofection,
CC   electroporation or restriction enzyme mediated integration. Also
CC   described: (1) a transgenic avian that produces at least one heterologous
CC   polypeptide in egg white, where the transgenic avian or founder ancestor
CC   of the transgenic avian was not produced using a eukaryotic viral vector;
CC   (2) a transgenic avian produced by the method above; (3) an avian egg
CC   produced by the transgenic avian; and (4) a heterologous protein produced
CC   by the transgenic avian, where the heterologous protein comprises a
CC   heterologous polypeptide selected from a cytokine, a hormone, an enzyme,
CC   a structural protein, and an immunoglobulin. The method is useful for
CC   generating a transgenic avian zygote and animals, which may be used in
CC   the production of heterologous proteins. The method is also useful in
CC   expressing in large yields and at low cost, a wide range of desired
CC   proteins including those used as human and animal pharmaceuticals,
CC   diagnostics, and livestock feed additives. The present sequence
CC   represents the SV40 polyadenylation signal sequence, which is given in
CC   the exemplification of the present invention
XX
SQ   Sequence 285 BP; 92 A; 46 C; 68 G; 79 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 9;  Length 285;
  Best Local Similarity   98.6%;  Pred. No. 7.9e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        111 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 170

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 230

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        231 CAAGTAAAACCTCTACAAATGTGGT 255


RESULT 11
ADV70462
ID   ADV70462 standard; DNA; 285 BP.
XX
AC   ADV70462;
XX
DT   24-FEB-2005  (first entry)
XX
DE   SV40 polyadenylation signal sequence.
XX
KW   MAR; matrix attachment region; ovalbumin;
KW   transcriptional regulatory element; avian cell;
KW   scaffold attachment region; SAR; polyA sequence; ds; SV40.
XX
OS   Simian virus 40.
XX
PN   WO2004094640-A1.
XX
PD   04-NOV-2004.
XX
PF   11-DEC-2003; 2003WO-US039244.
XX
PR   15-APR-2003; 2003US-0462953P.
PR   24-APR-2003; 2003US-0465215P.
PR   09-MAY-2003; 2003US-0469488P.
XX
PA   (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI   Ivarie R,  Leavitt MC,  Karnuah AB,  Rapp J,  Christmann L;
XX
DR   WPI; 2004-775942/76.
XX
PT   New nucleic acid molecule comprising an avian matrix attachment region
PT   and an avian ovalbumin transcriptional regulatory region, useful for
PT   reducing chromosomal positional effects or variations.
XX
PS   Disclosure; SEQ ID NO 2; 233pp; English.
XX
CC   The patent discloses isolated and recombinant nuclei acid molecules
CC   comprising at least one MAR (matrix attachment region) and an avian
CC   ovalbumin transcriptional regulatory element. The nucleic acid of the
CC   invention is useful in reducing the positional effects upon the
CC   transcription of a transgene operably linked to the ovalbumin
CC   transcriptional regulatory region and transfected into recipient avian
CC   cell. The recombinant nucleic acid molecules of the present invention may
CC   further comprise a polyadenylation signal sequence or an avian 3' domain,
CC   and optionally a internal ribosome entry site for expression of an
CC   operably linked heterologous nucleic acid insert in a transfected avian
CC   cell. The invention also relates to a method of generating a genetically
CC   transformed avian cell, a method of expressing a heterologous polypeptide
CC   in an avian cell, an avian cell, or its progeny thereof and a transgenic
CC   avian individual, where the avian egg white comprises a heterologous
```

CC polypeptide expressed from a recombinant nucleic acid molecule. The
CC preferred nucleic acid molecule includes a recombinant nucleic acid
CC molecule comprising an avian ovalbumin transcriptional regulatory region,
CC an avian 5' matrix attachment region, a heterologous nucleic acid
CC encoding a polypeptide, a polyadenylation signal sequence, and an avian
CC 3' matrix attachment region, where the avian ovalbumin transcriptional
CC regulatory control region, the 5' avian matrix attachment region, and the
CC avian 3' matrix attachment region independently hybridize under high
CC stringency conditions. The presence of matrix attachment region (MAR),
CC helps reduce the chromosome positional effect on the expression. MARs
CC also called as Scaffold attachment regions or SARs are regions that flank
CC either ends of a gene. Although MAR nucleic acid sequences are conserved
CC a little cross hybridization is seem, indicating significant overall
CC sequence variation. The preferred method includes, generating a
CC genetically transformed avian cell, by delivering the nucleotides of the
CC invention, into an avian cell under conditions where a genetically
CC transformed avian cell is generated. The avian cell is a chicken cell or
CC a quail cell. The avian cell is an oviduct cell, expressing a
CC heterologous polypeptide. The preferred transgenic avians include,
CC turkey, duck, goose, quail, pheasant, ratite, ornamental bird, or feral
CC bird, preferably chicken. The sequence presented here is the SV40
CC polyadenylation signal sequence.
XX
SQ Sequence 285 BP; 92 A; 46 C; 68 G; 79 T; 0 U; 0 Other;

Query Match 91.6%; Score 131; DB 13; Length 285;
Best Local Similarity 98.6%; Pred. No. 7.9e-27;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        111 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 170

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 230

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        231 CAAGTAAAACCTCTACAAATGTGGT 255
```

RESULT 12
AAV35371
ID AAV35371 standard; DNA; 296 BP.
XX
AC AAV35371;
XX
DT 09-OCT-1998 (first entry)
XX
DE Human INOS genomic DNA fragment #2.
XX
KW Inducible nitric oxide synthase; hiNOS; human; regulator; expression;
KW treatment; inflammation; sepsis; antitumour agent; inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO9812313-A1.
XX
PD 26-MAR-1998.
XX
PF 18-SEP-1997; 97WO-JP003303.
XX
PR 20-SEP-1996; 96JP-00250697.
XX
PA (SUNR) SUNTORY LTD.
XX
PI Nunokawa Y, Oikawa S, Tanaka S;
XX
DR WPI; 1998-230314/20.
XX
PT Screening for regulators of human inducible nitric oxide synthase
PT expression - using human cell line transformed with a reporter gene
PT flanked by 5'-promoter and 3'-non-translated regions of the hiNOS gene.
XX
PS Disclosure; Fig 3; 56pp; Japanese.
XX
CC This sequence is a fragment of human inducible nitric oxide synthase
CC (hiNOS) which can be used to screen for potential hiNOS expression
CC regulators. Such regulators have an effect on the modification of the
CC expression (in the presence of a cytokine inducer) of a reporter gene in
CC a human cell line transformed with an expression vector containing (in
CC order from 5'-end): the 5'-flanking region of the hiNOS gene containing
CC 544 bases, the reporter gene and the 3'-untranslated region of the hiNOS
CC gene. Suitable reporter genes include chloramphenicol acetyltransferase
CC (CAT), beta-galactosidase (beta -Gal) and luciferase. Compounds which
CC influence the expression of the hiNOS gene are useful for the treatment
CC of inflammation and sepsis, as antitumour agents and for the inhibition
CC of re-angio-stenosis, and other conditions involving abnormalities of
CC hiNOS expression
XX
SQ Sequence 296 BP; 94 A; 51 C; 68 G; 83 T; 0 U; 0 Other;

Query Match 91.6%; Score 131; DB 2; Length 296;
Best Local Similarity 98.6%; Pred. No. 7.9e-27;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        106 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 165

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 225

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        226 CAAGTAAAACCTCTACAAATGTGGT 250
```

RESULT 13
AAZ32097
ID AAZ32097 standard; DNA; 296 BP.
XX
AC AAZ32097;
XX
DT 11-JAN-2000 (first entry)
XX
DE pGL3 basic plasmid SV40 polyA nucleotide sequence.
XX
KW Human induced nitrogen monoxide synthase; hiNOS; untranslated region;
KW NF-kappaB; expression; activation; regulation; ds.
XX
OS Synthetic.
XX
PN JP11266872-A.
XX
PD 05-OCT-1999.
XX
PF 20-MAR-1998; 98JP-00090664.
XX
PR 20-MAR-1998; 98JP-00090664.
XX
PA (SUNR) SUNTORY LTD.
XX
DR WPI; 1999-613779/53.
XX
PT Method of screening a substance controlling activation of NF-kappaB -
PT having increased sensitivity.
XX
PS Disclosure; Fig 1; 16pp; Japanese.
XX
CC The present invention describes an expression-controlling sequence
CC containing a NF-kappaB recognising sequence, at least part of 3'-
CC untranslated region (3'-UTR) of human-induced nitrogen monoxide synthase
CC (hiNOS) and at least part of 3'-flanking region. Also described are: (a)

```
CC   an expression vector containing the above expression-controlling sequence
CC   ; (b) an expression vector containing (1) 5'-flanking region of hiNOS
CC   gene containing a promoter region, (2) a reporter gene and (3) the above
CC   expression-controlling sequence in this order from the 5'-side; (c) a
CC   cell transformed by the above expression vector; (d) a method for
CC   screening a substance controlling activation of NF-kappaB in which a cell
CC   which has the above expression-controlling sequence and can detect the
CC   activation of NF-kappaB is treated with a sample to observe the change in
CC   the expressed amount of the reporter gene; (e) a kit for screening a
CC   substance controlling activation of NF-kappaB containing the above cell;
CC   (f) a compound controlling activation of NF-kappaB prepared by using the
CC   above screening method; and (g) a drug composition for treating diseases
CC   caused by activation of NF-kappaB containing, with the above compound as
CC   the active component. The method can evaluate a compound controlling
CC   activation of NF-kappaB easily in a high sensitivity. The present
CC   sequence in used in the exemplification of the present invention
XX
SQ   Sequence 296 BP; 94 A; 51 C; 68 G; 83 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 2;  Length 296;
  Best Local Similarity   98.6%;  Pred. No. 7.9e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        106 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 165

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 225

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        226 CAAGTAAAACCTCTACAAATGTGGT 250


RESULT 14
ADW93253
ID   ADW93253 standard; DNA; 452 BP.
XX
AC   ADW93253;
XX
DT   07-APR-2005  (first entry)
XX
DE   SV40 DNA sequence #2.
XX
KW   parkinsons disease; gene therapy; ds.
XX
OS   Simian virus 40.
XX
PN   CN1429905-A.
XX
PD   16-JUL-2003.
XX
PF   04-JAN-2002; 2002CN-00100103.
XX
PR   04-JAN-2002; 2002CN-00100103.
XX
PA   (UYBE-) UNIV BEIJING.
XX
PI   Wang X,  Niu D,  Han J;
XX
DR   WPI; 2004-110052/12.
XX
PT   Recombination adenopathy adjoint virus carrier capable of controlling
PT   digene expression for treating parkinsonism.
XX
PS   Disclosure; Page 16; 20pp; Chinese.
XX
CC   The present invention relates to a novel adenovirus associated virus
CC   carrier for treating Parkinson's disease using tetracycline to induce the
CC   expression system. The adenovirus associated virus carrier carries and
CC   regulates human glial-derived neurotrophic factor (GDNF) and tyrosine
CC   hydroxylase (TH) genes. The adenovirus associated virus carrier has
CC   bidirectional promoter, two therapeutic genes (GDNF and TH) and
CC   regulatory element between two inverted terminal repeats (ITR). The
CC   method for introducing the said carrier in cells, screening and
CC   transplanting it in cerebral striate body or mixing with tetracycline
CC   transcriptional activator carrier for therapy is also disclosed. The
CC   present sequence was used to illustrate the invention.
XX
SQ   Sequence 452 BP; 117 A; 112 C; 116 G; 107 T; 0 U; 0 Other;

  Query Match             91.6%;  Score 131;  DB 13;  Length 452;
  Best Local Similarity   98.6%;  Pred. No. 8.6e-27;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db         76 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 135

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 195

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        196 CAAGTAAAACCTCTACAAATGTGGT 220


RESULT 15
ADY84551/c
ID   ADY84551 standard; DNA; 481 BP.
XX
AC   ADY84551;
XX
DT   16-JUN-2005  (first entry)
XX
DE   SV40 polyadenylation signal sequence.
XX
KW   DNA vaccine; ds; acquired immune deficiency syndrome; anti-hiv;
KW   immune disorder; HIV-1 infection; therapy.
XX
OS   Simian virus 40.
OS   Synthetic.
OS   Unidentified.
XX
PN   WO2005027844-A2.
XX
PD   31-MAR-2005.
XX
PF   16-SEP-2004; 2004WO-US030512.
XX
PR   16-SEP-2003; 2003US-0503197P.
PR   15-SEP-2004; 2004US-00941164.
XX
PA   (UNIV ) UNIV KANSAS MEDICAL CENT.
XX
PI   Narayan O,  Liu Z;
XX
DR   WPI; 2005-262643/27.
XX
PT   DNA vaccine for immunization against HIV, has isolated DNA molecule
PT   encoding viral proteins capable of stimulating immune response against
PT   HIV, and being unable to encode functional reverse transcriptase,
PT   integrase and Vif proteins.
XX
PS   Claim 46; SEQ ID NO 6; 124pp; English.
XX
CC   The invention relates to a DNA vaccine (I) for immunization against HIV
CC   comprising an isolated DNA molecule having a sequence encoding several
CC   viral proteins capable of stimulating an immune response against HIV,
CC   where the DNA molecule is unable to encode functional reverse
CC   transcriptase, integrase and Vif proteins, and further where a 3' long
CC   terminal repeat (LTR) of the DNA molecule is at least partially disrupted
CC   (i.e. rendered nonpathogenic by disruption of the rt gene, the int gene,
```

CC the vif gene, and the 3' long terminal repeat). The DNA vaccine (delta4-
CC SHIVku2) appears as ADY84546 and comprises the 5' LTR of Simian
CC immunodeficiency virus (SIV), the gag gene of HIV, the pro gene of HIV,
CC the vpx gene of SIV, the vpr gene of SIV, the nef gene of HIV, the tat
CC gene of HIV, the env gene of HIV, and an SV40 polyadenylation sequence.
CC Also included are a DNA vaccine construct for immunization against HIV
CC (comprising an isolated DNA molecule having a promoter sequence that is
CC operably linked to a sequence encoding several viral proteins capable of
CC stimulating an immune response against HIV, where the DNA molecule is
CC unable to encode functional reverse transcriptase, integrase and Vif
CC proteins and contains at least a partial disruption of the 3' long
CC terminal repeat of the DNA molecule, and which is operably linked to and
CC a polyadenylation sequence) and providing vaccination against HIV (or
CC treating an HIV-1 positive individual) involving administering to a
CC recipient the DNA composition comprising the. The DNA vaccine is useful
CC for providing vaccination against HIV. The method of vaccination further
CC involves administering to the recipient a cytokine. The vaccine and
CC methods are useful for treating an HIV-1 positive individual. The present
CC sequence represents the SV40 polyadenylation signal sequence used in the
CC DNA vaccine.
XX
SQ Sequence 481 BP; 139 A; 106 C; 82 G; 154 T; 0 U; 0 Other;

Query Match 91.6%; Score 131; DB 14; Length 481;
Best Local Similarity 98.6%; Pred. No. 8.7e-27;
Matches 143; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db        406 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 347

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db        346 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 287

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        286 CAAGTAAAACCTCTACAAATGTGGT 262
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Search completed: November 21, 2005, 23:36:21
Job time : 218.327 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:49:09 ; Search time 1226.1 Seconds
(without alignments)
6629.665 Million cell updates/sec

Title: US-10-683-775-1_COPY_80_222
Perfect score: 143
Sequence: 1 aatttgtgatgctattgctt.....aaaacctctacaaatgtggt 143

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
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5: gb_ov:*
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8: gb_pr:*
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12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	143	100.0	222	6	AR408763	AR408763 Sequence
c 2	143	100.0	222	6	AR408765	AR408765 Sequence
3	143	100.0	222	6	AX113060	AX113060 Sequence
c 4	143	100.0	222	6	AX113062	AX113062 Sequence
c 5	131	91.6	230	6	CS070728	CS070728 Sequence
c 6	131	91.6	230	6	AR179485	AR179485 Sequence
c 7	131	91.6	230	6	AR632154	AR632154 Sequence
8	131	91.6	296	6	AR142644	AR142644 Sequence
9	131	91.6	296	6	E28936	E28936 Method for
10	131	91.6	573	8	HSA332357	AJ332357 Homo sapi
11	131	91.6	667	6	AX114869	AX114869 Sequence
12	131	91.6	677	6	AR016495	AR016495 Sequence
13	131	91.6	677	6	AR096878	AR096878 Sequence
14	131	91.6	677	6	BD136073	BD136073 Vaccines
c 15	131	91.6	717	6	AR476069	AR476069 Sequence
c 16	131	91.6	717	6	BD002329	BD002329 Transgeni
17	131	91.6	770	6	AX114868	AX114868 Sequence
c 18	131	91.6	782	6	AR310572	AR310572 Sequence
c 19	131	91.6	782	6	AX150253	AX150253 Sequence
20	131	91.6	826	6	E01619	E01619 DNA sequenc
c 21	131	91.6	1078	6	A92081	A92081 Sequence 5
c 22	131	91.6	1078	6	AR230688	AR230688 Sequence
c 23	131	91.6	1096	11	AY590429	AY590429 Cloning v
c 24	131	91.6	1318	6	A92080	A92080 Sequence 4
c 25	131	91.6	1318	6	AR230690	AR230690 Sequence
c 26	131	91.6	1417	6	A92077	A92077 Sequence 1
c 27	131	91.6	1417	6	AR230692	AR230692 Sequence
28	131	91.6	1433	6	CQ971831	CQ971831 Sequence
c 29	131	91.6	1447	11	AF140802	AF140802 Expressio
c 30	131	91.6	1513	11	AF140800	AF140800 Expressio
c 31	131	91.6	1513	11	AF140801	AF140801 Expressio
32	131	91.6	1578	6	CS038903	CS038903 Sequence
c 33	131	91.6	1645	6	A92078	A92078 Sequence 2
c 34	131	91.6	1645	6	AR230689	AR230689 Sequence
c 35	131	91.6	1723	11	SYNIL2S	L78438 Synthetic S
c 36	131	91.6	1798	6	CQ871823	CQ871823 Sequence
c 37	131	91.6	1798	6	CQ871841	CQ871841 Sequence
c 38	131	91.6	1798	6	CQ872311	CQ872311 Sequence
c 39	131	91.6	1870	6	A92079	A92079 Sequence 3
c 40	131	91.6	1870	6	AR230691	AR230691 Sequence
c 41	131	91.6	2143	11	SYNDSP2	K03394 Synthetic p
42	131	91.6	2197	6	CQ971825	CQ971825 Sequence
43	131	91.6	2420	6	CS131149	CS131149 Sequence
c 44	131	91.6	2792	6	BD231755	BD231755 Transgeni
c 45	131	91.6	2792	6	AR392743	AR392743 Sequence

ALIGNMENTS

RESULT 1
AR408763
LOCUS AR408763 222 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6632637.
ACCESSION AR408763
VERSION AR408763.1 GI:40159158
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 222)
AUTHORS McGrew,J.T.
TITLE Vectors and methods for recombinant protein expression
JOURNAL Patent: US 6632637-A 1 14-OCT-2003;
Immunex Corporation; Seattle, WA
FEATURES Location/Qualifiers
source 1. .222
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 143; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 60
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Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
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Qy        121 AGTAAAACCTCTACAAATGTGGT 143
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Db        200 AGTAAAACCTCTACAAATGTGGT 222
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LOCUS AR408765 222 bp DNA linear PAT 18-DEC-2003

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DEFINITION  Sequence 3 from patent US 6632637.
ACCESSION   AR408765
VERSION     AR408765.1  GI:40159160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 222)
  AUTHORS   McGrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: US 6632637-A 3 14-OCT-2003;
            Immunex Corporation; Seattle, WA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 60
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Db        143 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 84

Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 24

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||
Db         23 AGTAAAACCTCTACAAATGTGGT 1


RESULT 3
AX113060
LOCUS       AX113060                222 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 1 from Patent WO0127299.
ACCESSION   AX113060
VERSION     AX113060.1  GI:13939494
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Mcgrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: WO 0127299-A 1 19-APR-2001;
            Immunex CorporatioN (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10633"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.7e-24;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
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Db        140 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 199

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
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Db        200 AGTAAAACCTCTACAAATGTGGT 222


RESULT 4
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LOCUS       AX113062                222 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 3 from Patent WO0127299.
ACCESSION   AX113062
VERSION     AX113062.1  GI:13939496
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Mcgrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: WO 0127299-A 3 19-APR-2001;
            Immunex CorporatioN (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTCAACA 84

Qy         61 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCA 24

Qy        121 AGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||
Db         23 AGTAAAACCTCTACAAATGTGGT 1


RESULT 5
CS070728/c
LOCUS       CS070728                230 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 1 from Patent WO2001034815.
ACCESSION   CS070728
VERSION     CS070728.1  GI:63088136
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Liu,L., Chouinard,S. and Velema,J.
  TITLE     dsRNA as insect control agent
  JOURNAL   Patent: WO 2001034815-A 1 17-MAY-2001;
            Cambria Biosciences, LLC (US)
FEATURES             Location/Qualifiers
     source          1. .230
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence:SV 40
                     Transcriptional Terminator Sequence"
ORIGIN

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  Best Local Similarity   98.6%;  Pred. No. 1.4e-21;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        162 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 103

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 43

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
                 |||||||||||||||||||||||||
Db         42 CAAGTAAAACCTCTACAAATGTGGT 18


RESULT 6
AR179485/c
LOCUS       AR179485                 230 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1 from patent US 6326193.
ACCESSION   AR179485
VERSION     AR179485.1  GI:20221040
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   Liu,L., Chouinard,S. and Velema,J.
  TITLE     Insect control agent
  JOURNAL   Patent: US 6326193-A 1 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .230
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ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 230;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-21;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        162 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 103

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 43

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
                 |||||||||||||||||||||||||
Db         42 CAAGTAAAACCTCTACAAATGTGGT 18


RESULT 7
AR632154/c
LOCUS       AR632154                 230 bp    DNA     linear   PAT 14-FEB-2005
DEFINITION  Sequence 1 from patent US 6846482.
ACCESSION   AR632154
VERSION     AR632154.1  GI:59776097
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   Liu,L., Chouinard,S. and Velema,J.
  TITLE     Insect control agent
  JOURNAL   Patent: US 6846482-A 1 25-JAN-2005;
            Cambria Biosciences; Woburn, MA
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     source          1. .230
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ORIGIN

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  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db         42 CAAGTAAAACCTCTACAAATGTGGT 18


RESULT 8
AR142644
LOCUS       AR142644                 296 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6203982.
ACCESSION   AR142644
VERSION     AR142644.1  GI:15103930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 296)
  AUTHORS   Nunokawa,Y., Oikawa,S. and Tanaka,S.
  TITLE     Method for screening compounds regulating the expression of
            human-inducible nitric oxide synthase
  JOURNAL   Patent: US 6203982-A 2 20-MAR-2001;
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ORIGIN

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Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db        166 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 225

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        226 CAAGTAAAACCTCTACAAATGTGGT 250


RESULT 9
E28936
LOCUS       E28936                   296 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for screening NF-kappa-B activation inhibitor.
ACCESSION   E28936
VERSION     E28936.1  GI:13020928
KEYWORDS    JP 1999266872-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 296)
  AUTHORS   Yoichi,F.
  TITLE     Method for screening NF-kappa-B activation inhibitor
  JOURNAL   Patent: JP 1999266872-A 1 05-OCT-1999;
            SUNTORY LTD
COMMENT     OS   Unidentified
            PN   JP 1999266872-A/1
            PD   05-OCT-1999
            PF   20-MAR-1998 JP 1998090664
            PR
            PI   YOICHI FUKAWA
            PC   C12N15/09,A61K38/00,A61K45/00,C12N5/10,C12Q1/68, PC
            G01N33/15//C07D295/10,
            PC   (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),C12N15/00,A61K37/02,
            PC   C12N5/00,
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            FH   Key             Location/Qualifiers
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Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        226 CAAGTAAAACCTCTACAAATGTGGT 250


RESULT 10
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LOCUS       HSA332357               573 bp    DNA     linear   PRI 18-JUL-2002
DEFINITION  Homo sapiens genomic sequence surrounding NotI site, clone
            HSJ4P-P16RS.
ACCESSION   AJ332357
VERSION     AJ332357.1  GI:15876775
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
            Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
  TITLE     NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
  JOURNAL   Nucleic Acids Res. 30 (14), 3163-3170 (2002)
   PUBMED   12136098
REFERENCE   2  (bases 1 to 573)
  AUTHORS   Zabarovsky,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .573
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                     /clone="HSJ4P-P16RS"
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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db        166 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 225

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        226 CAAGTAAAACCTCTACAAATGTGGT 250


RESULT 11
AX114869
LOCUS       AX114869                667 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 29 from Patent WO0129208.
ACCESSION   AX114869
VERSION     AX114869.1  GI:14031811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 29 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA sequence derived from vector pRK80c"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 667;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-21;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        408 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 467

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 527

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        528 CAAGTAAAACCTCTACAAATGTGGT 552


RESULT 12
AR016495
LOCUS       AR016495                677 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5776746.
ACCESSION   AR016495
VERSION     AR016495.1  GI:3972772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Denney,D.W. Jr.
  TITLE     Gene amplification methods
  JOURNAL   Patent: US 5776746-A 3 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 677;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-21;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;
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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db         82 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 141

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Db        142 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 201

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        202 CAAGTAAAACCTCTACAAATGTGGT 226


RESULT 13
AR096878
LOCUS       AR096878                677 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 3 from patent US 5972334.
ACCESSION   AR096878
VERSION     AR096878.1  GI:10009402
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Denney,D.W. Jr.
  TITLE     Vaccines for treatment of lymphoma and leukemia
  JOURNAL   Patent: US 5972334-A 3 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="unknown"
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ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 677;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-21;
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Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db         82 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 141

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
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Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
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Db        202 CAAGTAAAACCTCTACAAATGTGGT 226


RESULT 14
BD136073
LOCUS       BD136073                677 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vaccines for treatment of lymphoma and leukemia.
ACCESSION   BD136073
VERSION     BD136073.1  GI:23231018
KEYWORDS    JP 2002509426-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Jr,D.W.D.
  TITLE     Vaccines for treatment of lymphoma and leukemia
  JOURNAL   Patent: JP 2002509426-A 3 26-MAR-2002;
            GENITOPE CORP
COMMENT     OS   Unidentified
            PN   JP 2002509426-A/3
            PD   26-MAR-2002
            PF   25-APR-1997 JP 1997539097
            PR   01-MAY-1996 US    08/644664,06-DEC-1996 US    08/761277 PI
            DAN W DENNEY JR
            PC   C12N15/86,C12N15/63,C12N15/00,C12P19/24,A61K39/395,C07H21/04
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   Vaccines for treatment of lymphoma and leukemia FH   Key
                  Location/Qualifiers
            FT   source          1. .677
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   98.6%;  Pred. No. 1.1e-21;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db         82 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 141

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 201

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        202 CAAGTAAAACCTCTACAAATGTGGT 226


RESULT 15
AR476069/c
LOCUS       AR476069                717 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 3 from patent US 6693226.
ACCESSION   AR476069
VERSION     AR476069.1  GI:42716014
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   McNeish,J.D. and Ahlijanian,M.K.
  TITLE     Transgenic mice expressing human p25
  JOURNAL   Patent: US 6693226-A 3 17-FEB-2004;
            Pfizer Inc; New York, NY
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             91.6%;  Score 131;  DB 6;  Length 717;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-21;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTT--CAA 58
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Db        636 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA 577

Qy         59 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAG 517

Qy        119 CAAGTAAAACCTCTACAAATGTGGT 143
              |||||||||||||||||||||||||
Db        516 CAAGTAAAACCTCTACAAATGTGGT 492


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GenCore version 5.1.6
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SUMMARIES

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	3	210	94.6	677	2	US-08-644-664B-3	Sequence 3, Appli
	4	210	94.6	677	2	US-08-761-277A-3	Sequence 3, Appli
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c	11	210	94.6	3822	3	US-08-675-566-8	Sequence 8, Appli
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	15	210	94.6	4059	2	US-08-564-313-2	Sequence 2, Appli
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c	19	210	94.6	4273	3	US-08-601-132-37	Sequence 37, Appl
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	23	210	94.6	4455	2	US-08-474-169-5	Sequence 5, Appli
c	24	210	94.6	4503	3	US-08-675-566-7	Sequence 7, Appli
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c	27	210	94.6	4810	2	US-08-453-552-7	Sequence 7, Appli
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c	30	210	94.6	4810	6	PCT-US94-07280-3	Sequence 3, Appli
c	31	210	94.6	4810	6	PCT-US95-01087-3	Sequence 3, Appli
	32	210	94.6	4963	2	US-08-076-716-16	Sequence 16, Appl
	33	210	94.6	4963	2	US-08-260-452-9	Sequence 9, Appli
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	35	210	94.6	4963	2	US-08-897-719-9	Sequence 9, Appli
	36	210	94.6	4963	3	US-09-163-269-9	Sequence 9, Appli
	37	210	94.6	4963	3	US-09-281-674-9	Sequence 9, Appli
	38	210	94.6	4963	3	US-09-777-317B-9	Sequence 9, Appli
	39	210	94.6	4990	3	US-08-776-511-1	Sequence 1, Appli
c	40	210	94.6	5030	2	US-08-588-201-14	Sequence 14, Appl
c	41	210	94.6	5030	2	US-09-169-605-14	Sequence 14, Appl
c	42	210	94.6	5030	3	US-08-893-327-14	Sequence 14, Appl
c	43	210	94.6	5067	3	US-08-675-566-20	Sequence 20, Appl
c	44	210	94.6	5125	2	US-08-453-552-11	Sequence 11, Appl
c	45	210	94.6	5125	2	US-08-710-637-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-687-050-1
; Sequence 1, Application US/09687050
; Patent No. 6632637
; GENERAL INFORMATION:
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: VECTORS AND METHODS FOR RECOMBINANT PROTEIN EXPRESSION
; FILE REFERENCE: 2902-A
; CURRENT APPLICATION NUMBER: US/09/687,050
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,177
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 222
; TYPE: DNA
; ORGANISM: SV40
US-09-687-050-1

Query Match 100.0%; Score 222; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 8.1e-50;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
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RESULT 2
US-09-687-050-3/c
; Sequence 3, Application US/09687050
; Patent No. 6632637
; GENERAL INFORMATION:
; APPLICANT: McGrew, Jeffrey T.

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;  TITLE OF INVENTION:   VECTORS AND METHODS FOR RECOMBINANT PROTEIN EXPRESSION
;  FILE REFERENCE:   2902-A
;  CURRENT APPLICATION NUMBER: US/09/687,050
;  CURRENT FILING DATE:  2000-10-12
;  PRIOR APPLICATION NUMBER:   60/159,177
;  PRIOR FILING DATE:   1999-10-13
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 222
;   TYPE: DNA
;   ORGANISM: SV40
US-09-687-050-3

  Query Match             100.0%;  Score 222;  DB 3;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-50;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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RESULT 3
US-08-644-664B-3
; Sequence 3, Application US/08644664B
; Patent No. 5776746
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Gene Amplication Methods
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/644,664B
;      FILING DATE:  01-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  GENITOPE-00912
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  677 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-644-664B-3

  Query Match             94.6%;  Score 210;  DB 2;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
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Db        123 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 182

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              |||||||||||||||||||||||||||||||||||||||||||
Db        183 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 226


RESULT 4
US-08-761-277A-3
; Sequence 3, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  677 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-761-277A-3

  Query Match             94.6%;  Score 210;  DB 2;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          3 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 62

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 122

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 182

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        183 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 226


RESULT 5
US-09-496-445-3/c
; Sequence 3, Application US/09496445
; Patent No. 6693226
; GENERAL INFORMATION:
;  APPLICANT: McNeish, John D.
;  APPLICANT: Ahlijnian, Michael K
;  TITLE OF INVENTION: Transgenic Animals Expressing Human p25
;  FILE REFERENCE: PC10142A
;  CURRENT APPLICATION NUMBER: US/09/496,445
;  CURRENT FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Rous sarcoma virus
US-09-496-445-3

  Query Match             94.6%;  Score 210;  DB 3;  Length 717;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 656

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 596

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        595 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 536

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        535 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 492


RESULT 6
US-09-714-550-8/c
; Sequence 8, Application US/09714550
; Patent No. 6558948
; GENERAL INFORMATION:
;  APPLICANT: Kochanek, Stefan
;  APPLICANT:  Schiedner, Gudrun
;  TITLE OF INVENTION: Permanent amniocytic cell line, its
;  TITLE OF INVENTION:  production and use for the production of gene transfer
;  TITLE OF INVENTION:  vectors
;  FILE REFERENCE: 50125/007002
;  CURRENT APPLICATION NUMBER: US/09/714,550
;  CURRENT FILING DATE:  2000-11-16
;  PRIOR APPLICATION NUMBER: US 60/167,439
;  PRIOR FILING DATE: 1999-11-23
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-09-714-550-8

  Query Match             94.6%;  Score 210;  DB 3;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 716

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 656

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        655 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 596

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        595 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 552


RESULT 7
US-08-994-689C-8/c
; Sequence 8, Application US/08994689C
; Patent No. 6613958
;  GENERAL INFORMATION:
;    APPLICANT:  Neuhold, Lisa
;    APPLICANT:  Killar, Loran
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL MODEL FOR
;    TITLE OF INVENTION:  DEGENERATIVE DISEASES OF CARTILAGE
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/994,689C
;      FILING DATE:  1997-12-19
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Reza
;      REGISTRATION NUMBER:  38,475
;      REFERENCE/DOCKET NUMBER:  0630/0D532
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2792 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-994-689C-8
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  Query Match             94.6%;  Score 210;  DB 3;  Length 2792;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2758 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 2699

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2698 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 2639

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       2638 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 2579

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       2578 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 2535


RESULT 8
US-09-496-445-4/c
; Sequence 4, Application US/09496445
; Patent No. 6693226
; GENERAL INFORMATION:
;  APPLICANT: McNeish, John D.
;  APPLICANT: Ahlijnian, Michael K
;  TITLE OF INVENTION: Transgenic Animals Expressing Human p25
;  FILE REFERENCE: PC10142A
;  CURRENT APPLICATION NUMBER: US/09/496,445
;  CURRENT FILING DATE: 2000-02-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 3218
;   TYPE: DNA
;   ORGANISM: Multi organism source
US-09-496-445-4

  Query Match             94.6%;  Score 210;  DB 3;  Length 3218;
  Best Local Similarity   99.1%;  Pred. No. 2.3e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3216 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 3157

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3156 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 3097

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       3096 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 3037

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       3036 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 2993


RESULT 9
US-08-169-613A-1/c
; Sequence 1, Application US/08169613A
; Patent No. 6486380
; GENERAL INFORMATION:
;  APPLICANT: Epstein, Paul
;  TITLE OF INVENTION: Pancreatic B Cell Hexokinase Transgene
;  FILE REFERENCE: P0044US0
;  CURRENT APPLICATION NUMBER: US/08/169,613A
;  CURRENT FILING DATE:  1993-12-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3318
;   TYPE: DNA
;   ORGANISM: yeast
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (790)..(2247)
US-08-169-613A-1

  Query Match             94.6%;  Score 210;  DB 3;  Length 3318;
  Best Local Similarity   99.1%;  Pred. No. 2.3e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3260 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 3201

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3200 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 3141

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       3140 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 3081

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       3080 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 3037


RESULT 10
US-08-955-565A-6
; Sequence 6, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
;  APPLICANT: Malkovsky, Miroslav
;  APPLICANT:  Wells, Andrew
;  TITLE OF INVENTION: Immune Response Enhancer Therapy
;  FILE REFERENCE: WARF-02625
;  CURRENT APPLICATION NUMBER: US/08/955,565A
;  CURRENT FILING DATE:  1997-10-17
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 3740
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-08-955-565A-6

  Query Match             94.6%;  Score 210;  DB 3;  Length 3740;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 1243

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1303

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 1363

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1364 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1407
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RESULT 11
US-08-675-566-8/c
; Sequence 8, Application US/08675566
; Patent No. 6090393
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Laurent
;    TITLE OF INVENTION:  PROMOTERS, EXPRESSION CASSETTES,
;    TITLE OF INVENTION:  RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,566
;      FILING DATE:  03-JUL-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2890
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)840-3333
;      TELEFAX:  (212)840-0712
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3822 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-675-566-8

  Query Match             94.6%;  Score 210;  DB 3;  Length 3822;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 1066

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1006

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1005 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 946

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        945 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 902


RESULT 12
US-07-678-408A-1/c
; Sequence 1, Application US/07678408A
; Patent No. 5266490
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Sam
;    APPLICANT:  Yancopoulos, George D.
;    TITLE OF INVENTION:  Mammalian Expression Vector
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  N.Y.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/678,408A
;      FILING DATE:  19910328
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S.Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  6526-052-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 869-9741
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3944 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
US-07-678-408A-1

  Query Match             94.6%;  Score 210;  DB 2;  Length 3944;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 1917

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1857

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1856 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 1797

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1796 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1753


RESULT 13
US-08-675-566-10/c
; Sequence 10, Application US/08675566
; Patent No. 6090393
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Laurent
;    TITLE OF INVENTION:  PROMOTERS, EXPRESSION CASSETTES,
;    TITLE OF INVENTION:  RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,566
```

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;       FILING DATE:  03-JUL-1996
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer Esq., William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2890
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)840-3333
;       TELEFAX:  (212)840-0712
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3955 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-675-566-10

  Query Match             94.6%;  Score 210;  DB 3;  Length 3955;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 1199

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1139

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1138 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 1079

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1078 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1035


RESULT 14
US-08-675-566-9/c
; Sequence 9, Application US/08675566
; Patent No. 6090393
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Laurent
;    TITLE OF INVENTION:  PROMOTERS, EXPRESSION CASSETTES,
;    TITLE OF INVENTION:  RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,566
;      FILING DATE:  03-JUL-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2890
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)840-3333
;      TELEFAX:  (212)840-0712
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  4009 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-675-566-9

  Query Match             94.6%;  Score 210;  DB 3;  Length 4009;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-46;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 1253

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1193

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1192 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 1133

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1132 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1089


RESULT 15
US-08-564-313-2
; Sequence 2, Application US/08564313
; Patent No. 5910488
;  GENERAL INFORMATION:
;    APPLICANT:  Nabel, Elizabeth
;    APPLICANT:  Nabel, Gary
;    APPLICANT:  Lew, Denise
;    APPLICANT:  Marquet, Magda
;    TITLE OF INVENTION:  PLASMIDS SUITABLE FOR GENE THERAPY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson and Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/564,313
;      FILING DATE:  01-DEC-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/074,344
;      FILING DATE:  07-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  VICAL.033CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4059 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  cDNA
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7
US-08-564-313-2

Query Match 94.6%; Score 210; DB 2; Length 4059;
Best Local Similarity 99.1%; Pred. No. 2.4e-46;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 1236

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1296

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1297 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 1356

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1357 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1400
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Search completed: November 22, 2005, 01:25:57
Job time : 102.221 secs

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:53:25 ; Search time 2382.62 Seconds
(without alignments)
4359.368 Million cell updates/sec

Title: US-10-683-775-1
Perfect score: 222
Sequence: 1 atccagacatgataagatac.....aaaacctctacaaatgtggt 222

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	210	94.6	278	6	CD282637	CD282637 G38935.14
c 2	210	94.6	334	7	CV006397	CV006397 CS_gil_12
c 3	210	94.6	353	6	CD279996	CD279996 G43757.10
c 4	210	94.6	372	1	AL039087	AL039087 DKFZp566H
c 5	210	94.6	380	7	CV161679	CV161679 CS_gil_54
6	210	94.6	395	3	BP420484	BP420484 BP420484
c 7	210	94.6	429	6	CD281635	CD281635 G43981.18
c 8	210	94.6	430	7	CV527659	CV527659 CS_GIL_06
9	210	94.6	431	3	BP426053	BP426053 BP426053
10	210	94.6	455	3	BP418262	BP418262 BP418262
11	210	94.6	461	3	BP418191	BP418191 BP418191
c 12	210	94.6	464	6	CD280357	CD280357 G43757.71
c 13	210	94.6	495	7	CV526695	CV526695 CS_GIL_17
14	210	94.6	503	3	BP420735	BP420735 BP420735
15	210	94.6	507	3	BP420280	BP420280 BP420280
c 16	210	94.6	507	6	CD280879	CD280879 G43756.65
c 17	210	94.6	526	7	CV463249	CV463249 CS_hyp_55
c 18	210	94.6	530	7	CV527488	CV527488 CS_GIL_12
c 19	210	94.6	531	7	CV006382	CV006382 CS_gil_12
c 20	210	94.6	534	7	CV071227	CV071227 CS_gil_39
c 21	210	94.6	549	6	CD280355	CD280355 G44283.63
c 22	210	94.6	558	6	CD280662	CD280662 G43520.61
c 23	210	94.6	573	6	CD281110	CD281110 G43828.86
c 24	210	94.6	593	6	CD281109	CD281109 G43756.86
c 25	210	94.6	615	1	AL037259	AL037259 DKFZp564B
c 26	210	94.6	625	7	CV086687	CV086687 CS_gil_46
c 27	210	94.6	644	7	CV161062	CV161062 CS_gil_57
c 28	210	94.6	672	7	CO392141	CO392141 WS#9_E03_
c 29	210	94.6	680	7	CV528133	CV528133 CS_GIL_16
c 30	210	94.6	684	6	CD281878	CD281878 G44220.23
c 31	210	94.6	686	7	CV030972	CV030972 CS_gil_27
c 32	210	94.6	709	7	CO392043	CO392043 WS#1_G03_
c 33	210	94.6	731	10	CG847851	CG847851 ZMMBBb031
c 34	210	94.6	768	10	CG848277	CG848277 ZMMBBb031
c 35	210	94.6	787	5	BU158260	BU158260 AGENCOURT
c 36	210	94.6	796	7	CO391849	CO391849 WS#1_G02_
c 37	210	94.6	960	7	CK629405	CK629405 AM1-AA001
c 38	210	94.6	1041	8	DR735602	DR735602 FGAS01545
c 39	210	94.6	1044	8	DR735960	DR735960 FGAS01825
c 40	210	94.6	1055	8	DR735606	DR735606 FGAS01554
c 41	210	94.6	1075	8	DR736123	DR736123 FGAS02060
c 42	210	94.6	1086	8	DR735943	DR735943 FGAS01788
c 43	210	94.6	1111	8	DR736126	DR736126 FGAS02066
c 44	210	94.6	1114	8	DR736237	DR736237 FGAS02229
c 45	210	94.6	1123	8	DR735948	DR735948 FGAS01797

ALIGNMENTS

RESULT 1
CD282637/c
LOCUS CD282637 278 bp mRNA linear EST 23-MAY-2003
DEFINITION G38935.14 NCI_CGAP_ZEmb2 Danio rerio cDNA clone IMAGE:6519507 5', mRNA sequence.
ACCESSION CD282637
VERSION CD282637.1 GI:31060413
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 278)
AUTHORS Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A., Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
TITLE Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rerio embryonic library
JOURNAL Unpublished (2003)
COMMENT Contact: Chen F.
Exelixis, Inc.
170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
Tel: 650 837 7000
Fax: 650 837 8300
Email: fchen@exelixis.com
DNA Sequencing by: Exelixis, Inc. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: 14103 row: L column: 3
High quality sequence stop: 278.
FEATURES Location/Qualifiers
source 1. .278
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6519507"
/tissue_type="embryo"
/lab_host="DH10B (T1-resistant)"
/clone_lib="NCI_CGAP_ZEmb2"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI_CGAP Library."
ORIGIN

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  Query Match             94.6%;  Score 210;  DB 6;  Length 278;
  Best Local Similarity   99.1%;  Pred. No. 3.1e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 198

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 138

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        137 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 78

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         77 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 34
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RESULT 2
CV006397/c
LOCUS CV006397 334 bp mRNA linear EST 18-AUG-2004
DEFINITION CS_gil_12H12_M13Reverse Blue crab gill, normalized Callinectes sapidus cDNA clone CS_gil_12H12 5' similar to prf|1103278B ORF. Score = 89.0 bits (219), Expect = 3e-17, mRNA sequence.
ACCESSION CV006397
VERSION CV006397.1 GI:51365620
KEYWORDS EST.
SOURCE Callinectes sapidus (blue crab)
ORGANISM Callinectes sapidus
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE 1 (bases 1 to 334)
AUTHORS Shafer,T.H., Coblentz,F.E. and Towle,D.W.
TITLE Expressed sequence tags from normalized cDNA libraries prepared from gill and hypodermis tissues of the blue crab, Callinectes sapidus
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas H. Shafer
Department of Biological Sciences
University of North Carolina Wilmington
601 S. College Rd, Wilmington, NC 28403, USA
Tel: 910-962-7275
Fax: 910-962-4066
Email: shafert@uncw.edu
Plate: 12 row: H column: 12
Seq primer: M13 Reverse
High quality sequence stop: 324.

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FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_gil_12H12"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen. Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington. Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN
```

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  Query Match             94.6%;  Score 210;  DB 7;  Length 334;
  Best Local Similarity   99.1%;  Pred. No. 3.1e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db        302 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 243

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 183

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        182 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 123

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        122 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 79
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RESULT 3
CD279996/c
LOCUS CD279996 353 bp mRNA linear EST 23-MAY-2003
DEFINITION G43757.10 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6321722 5', mRNA sequence.
ACCESSION CD279996
VERSION CD279996.1 GI:31057772
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 353)
AUTHORS Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A., Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
TITLE Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio embryonic library
JOURNAL Unpublished (2003)
COMMENT Contact: Chen F.
Exelixis, Inc.
170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
Tel: 650 837 7000
Fax: 650 837 8300
Email: fchen@exelixis.com
DNA Sequencing by: Exelixis, Inc. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: 13762 row: C column: 3
High quality sequence stop: 353.

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FEATURES             Location/Qualifiers
     source          1. .353
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6321722"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN
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  Query Match             94.6%;  Score 210;  DB 6;  Length 353;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;
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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db        305 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 246

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 186

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        185 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 126

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        125 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 82
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RESULT 4
AL039087/c
LOCUS AL039087 372 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp566H204_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566H204 3', mRNA sequence.
ACCESSION AL039087
VERSION AL039087.1 GI:5408188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
No r1 sequence available.
This clone (DKFZp566H204) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
source 1. .372
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566H204"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
ORIGIN

Query Match 94.6%; Score 210; DB 1; Length 372;
Best Local Similarity 99.1%; Pred. No. 3.2e-41;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db        357 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 298

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 238

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        237 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        177 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 134
```

RESULT 5
CV161679/c
LOCUS CV161679 380 bp mRNA linear EST 08-SEP-2004
DEFINITION CS_gil_54H02_M13Reverse Blue crab gill, normalized Callinectes sapidus cDNA clone CS_gil_54H02 5' similar to prf|1103278B ORF. Score = 60.8 bits (146), Expect = 9e-09, mRNA sequence.
ACCESSION CV161679
VERSION CV161679.1 GI:51946943
KEYWORDS EST.
SOURCE Callinectes sapidus (blue crab)
ORGANISM Callinectes sapidus
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE 1 (bases 1 to 380)
AUTHORS Shafer,T.H., Coblentz,P.E. and Towle,D.W.
TITLE Expressed sequence tags from normalized cDNA libraries prepared from gill and hypodermis tissues of the blue crab, Callinectes sapidus
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas H. Shafer
Department of Biological Sciences
University of North Carolina Wilmington
601 S. College Rd, Wilmington, NC 28403, USA
Tel: 910-962-7275
Fax: 910-962-4066
Email: shafert@uncw.edu
Plate: 54 row: H column: 02
Seq primer: M13 Reverse
High quality sequence stop: 350.
FEATURES Location/Qualifiers
source 1. .380
/organism="Callinectes sapidus"
/mol_type="mRNA"
/db_xref="taxon:6763"
/clone="CS_gil_54H02"
/tissue_type="Pooled anterior and posterior gills from crabs acclimated to salinities of 35 and 5 parts per thousand"
/dev_stage="Adult intermolt"
/clone_lib="Blue crab gill, normalized"
/note="Vector: pCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, and then pooled for construction and normalization of a cDNA library by Invitrogen. Plasmids were isolated and inserts sequenced from their 5'-ends by the Blue Crab Molecular Genetics Laboratory at the University of North Carolina Wilmington. Traces were trimmed, compared (BLASTx) to NCBI non-redundant protein database as of 19 July 2004, and processed for submission to dbEST by trace2dbEST software (Parkinson, Anthony and Blaxter, unpublished software)."
ORIGIN

Query Match 94.6%; Score 210; DB 7; Length 380;
Best Local Similarity 99.1%; Pred. No. 3.2e-41;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 195

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 135

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        134 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 75

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         74 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 31


RESULT 6
BP420484
LOCUS       BP420484                 395 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420484 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE03774r 3', mRNA sequence.
ACCESSION   BP420484
VERSION     BP420484.1  GI:66786737
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE03774r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 395;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         44 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 103

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 163

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        164 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 223

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        224 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 267


RESULT 7
CD281635/c
LOCUS       CD281635                 429 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43981.18 NCI_CGAP_ZEmb2 Danio rerio cDNA clone IMAGE:6319444 5',
            mRNA sequence.
ACCESSION   CD281635
VERSION     CD281635.1  GI:31059411
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13756  row: D  column: 5
            High quality sequence stop: 429.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6319444"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb2"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 429;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 303

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 243

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 183

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        182 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 139


RESULT 8
CV527659/c
LOCUS       CV527659                 430 bp    mRNA    linear   EST 07-OCT-2004
DEFINITION  CS_GIL_06H06_SP6 Blue crab gill, normalized Callinectes sapidus
            cDNA clone CS_GIL_06H06 5' similar to prf|1103278B ORF. Score =
            89.0 bits (219), Expect = 3e-17, mRNA sequence.
ACCESSION   CV527659
VERSION     CV527659.1  GI:53912038
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
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            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 06  row: H  column: 06
            Seq primer: SP6
            High quality sequence start: 7
            High quality sequence stop: 406.
FEATURES             Location/Qualifiers
     source          1. .430
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_GIL_06H06"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 7;  Length 430;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 370

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 310

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        309 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 250

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        249 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 206


RESULT 9
BP426053
LOCUS       BP426053                 431 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP426053 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE09943r 3', mRNA sequence.
ACCESSION   BP426053
VERSION     BP426053.1  GI:66792306
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE09943r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 431;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 166

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 226

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        227 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 286

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        287 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 330


RESULT 10
BP418262
LOCUS       BP418262                 455 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP418262 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE01346r 3', mRNA sequence.
ACCESSION   BP418262
VERSION     BP418262.1  GI:66784515
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Homo sapiens"
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE01346r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 455;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 127

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 187

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        188 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 247

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        248 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 291


RESULT 11
BP418191
LOCUS       BP418191                461 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP418191 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE01271r 3', mRNA sequence.
ACCESSION   BP418191
VERSION     BP418191.1  GI:66784444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .461
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE01271r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 461;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 162

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 222

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        223 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 282

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        283 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 326


RESULT 12
CD280357/c
LOCUS       CD280357                464 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G43757.71 NCI_CGAP_ZEmb3 Danio rerio cDNA clone IMAGE:6321976 5',
            mRNA sequence.
ACCESSION   CD280357
VERSION     CD280357.1  GI:31058133
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 464)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A.,
            Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZEmb3, a Danio rerio
            embryonic library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 13762  row: M  column: 17
            High quality sequence stop: 464.
FEATURES             Location/Qualifiers
     source          1. .464
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6321976"
                     /tissue_type="embryo"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZEmb3"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by J. Wang (Research Genetics,
                     Invitrogen Corp) from tissue donated by L. Zon (Harvard
                     University). Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 464;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 182

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 122

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 62

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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                 ||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 18


RESULT 13
CV526695/c
LOCUS       CV526695                495 bp    mRNA    linear   EST 07-OCT-2004
DEFINITION  CS_GIL_17C02_SP6 Blue crab gill, normalized Callinectes sapidus
            cDNA clone CS_GIL_17C02 5' similar to prf|1103278B ORF. Score =
            89.0 bits (219), Expect = 4e-17, mRNA sequence.
ACCESSION   CV526695
VERSION     CV526695.1  GI:53911074
KEYWORDS    EST.
SOURCE      Callinectes sapidus (blue crab)
  ORGANISM  Callinectes sapidus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
            Eubrachyura; Portunoidea; Portunidae; Callinectes.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Shafer,T.H., Coblentz,F.E. and Towle,D.W.
  TITLE     Expressed sequence tags from normalized cDNA libraries prepared
            from gill and hypodermis tissues of the blue crab, Callinectes
            sapidus
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas H. Shafer
            Department of Biological Sciences
            University of North Carolina Wilmington
            601 S. College Rd, Wilmington, NC 28403, USA
            Tel: 910-962-7275
            Fax: 910-962-4066
            Email: shafert@uncw.edu
            Plate: 17  row: C  column: 02
            Seq primer: SP6
            High quality sequence start: 3
            High quality sequence stop: 378.
FEATURES             Location/Qualifiers
     source          1. .495
                     /organism="Callinectes sapidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6763"
                     /clone="CS_GIL_17C02"
                     /tissue_type="Pooled anterior and posterior gills from
                     crabs acclimated to salinities of 35 and 5 parts per
                     thousand"
                     /dev_stage="Adult intermolt"
                     /clone_lib="Blue crab gill, normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, and then pooled for construction and
                     normalization of a cDNA library by Invitrogen.  Plasmids
                     were isolated and inserts sequenced from their 5'-ends by
                     the Blue Crab Molecular Genetics Laboratory at the
                     University of North Carolina Wilmington.  Traces were
                     trimmed, compared (BLASTx) to NCBI non-redundant protein
                     database as of 19 July 2004, and processed for submission
                     to dbEST by trace2dbEST software (Parkinson, Anthony and
                     Blaxter, unpublished software)."
ORIGIN

  Query Match            94.6%;  Score 210;  DB 7;  Length 495;
  Best Local Similarity  99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db        359 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 300

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 240

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||

Db        239 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 180

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              ||||||||||||||||||||||||||||||||||||||||||||
Db        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 136


RESULT 14
BP420735
LOCUS       BP420735                503 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420735 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE04048r 3', mRNA sequence.
ACCESSION   BP420735
VERSION     BP420735.1  GI:66786988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 503)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .503
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE04048r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match            94.6%;  Score 210;  DB 3;  Length 503;
  Best Local Similarity  99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 156

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 216

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||

Db        217 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 276

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              ||||||||||||||||||||||||||||||||||||||||||||
Db        277 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 320


RESULT 15
BP420280
LOCUS       BP420280                507 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BP420280 Homo sapiens small intestine Homo sapiens cDNA clone
            HIE03560r 3', mRNA sequence.
ACCESSION   BP420280
VERSION     BP420280.1  GI:66786533
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HIE03560r"
                     /tissue_type="small intestine"
                     /clone_lib="Homo sapiens small intestine"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 3;  Length 507;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-41;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 229

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 289

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        290 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 349

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        350 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 393


Search completed: November 22, 2005, 01:21:27
Job time : 2385.62 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 21:49:24 ; Search time 335.836 Seconds
(without alignments)
4405.602 Million cell updates/sec

Title: US-10-683-775-1
Perfect score: 222
Sequence: 1 atccagacatgataagatac.....aaaacctctacaaatgtggt 222

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	222	100.0	222	5	AAF30815	Aaf30815 SV40 late
c 2	222	100.0	222	5	AAF30816	Aaf30816 SV40 earl
3	210	94.6	250	8	ADA50602	Ada50602 SV40 poly
4	210	94.6	667	5	AAD04943	Aad04943 Insert se
5	210	94.6	677	2	AAT97157	Aat97157 SV40 poly
c 6	210	94.6	717	3	AAA74636	Aaa74636 Plasmid p
7	210	94.6	770	5	AAD04942	Aad04942 Insert se
c 8	210	94.6	782	5	AAH20736	Aah20736 SV40 DNA
c 9	210	94.6	816	14	ADV21047	Adv21047 4x-Polyad
c 10	210	94.6	816	14	ADY66741	Ady66741 4X-polyad
11	210	94.6	1193	6	AAL42929	Aal42929 Medaka ov
12	210	94.6	1223	4	AAL02861	Aal02861 Human rep
13	210	94.6	1359	4	AAS41785	Aas41785 Genomic s
14	210	94.6	1359	4	AAS41797	Aas41797 Genomic s
15	210	94.6	1359	4	AAS41878	Aas41878 Genomic s
16	210	94.6	1359	4	AAS41845	Aas41845 Genomic s
17	210	94.6	1359	4	AAS41831	Aas41831 Genomic s
18	210	94.6	1359	4	AAS41894	Aas41894 Genomic s
19	210	94.6	1359	4	AAK85458	Aak85458 Human imm
20	210	94.6	1359	4	AAK85525	Aak85525 Human imm
21	210	94.6	1359	4	AAK85475	Aak85475 Human imm
22	210	94.6	1359	4	AAK69632	Aak69632 Human imm
23	210	94.6	1359	4	AAK85508	Aak85508 Human imm
24	210	94.6	1359	4	AAK69645	Aak69645 Human imm
25	210	94.6	1359	4	AAL02859	Aal02859 Human rep
26	210	94.6	1359	4	AAL02903	Aal02903 Human rep
27	210	94.6	1359	4	AAL02870	Aal02870 Human rep
28	210	94.6	1362	4	AAS41789	Aas41789 Genomic s
29	210	94.6	1362	4	AAS41882	Aas41882 Genomic s
30	210	94.6	1362	4	AAS41833	Aas41833 Genomic s
31	210	94.6	1362	4	AAK69636	Aak69636 Human imm
32	210	94.6	1362	4	AAK85462	Aak85462 Human imm
33	210	94.6	1362	4	AAK85512	Aak85512 Human imm
34	210	94.6	1362	4	AAL02864	Aal02864 Human rep
35	210	94.6	1423	4	AAS41787	Aas41787 Genomic s
36	210	94.6	1423	4	AAS41832	Aas41832 Genomic s
37	210	94.6	1423	4	AAS41880	Aas41880 Genomic s
38	210	94.6	1423	4	AAK69634	Aak69634 Human imm
39	210	94.6	1423	4	AAK85510	Aak85510 Human imm
40	210	94.6	1423	4	AAK85460	Aak85460 Human imm
41	210	94.6	1423	4	AAL02862	Aal02862 Human rep
42	210	94.6	1423	4	AAL02896	Aal02896 Human rep
43	210	94.6	1424	4	AAS41801	Aas41801 Genomic s
44	210	94.6	1424	4	AAS41853	Aas41853 Genomic s
45	210	94.6	1424	4	AAS41849	Aas41849 Genomic s

ALIGNMENTS

RESULT 1
AAF30815
ID AAF30815 standard; DNA; 222 BP.
XX
AC AAF30815;
XX
DT 21-JUN-2001 (first entry)
XX
DE SV40 late polyadenylation site.
XX
KW SV40; polyadenylation; vector; ss.
XX
OS Rhesus macaque polyoma virus.
XX
FH Key Location/Qualifiers
FT polyA_signal 123. .128
FT /*tag= a
FT misc_feature 151. .187
FT /*tag= b
FT /note= "G/T rich region"
XX
PN WO200127299-A1.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028431.
XX
PR 13-OCT-1999; 99US-0159177P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Mcgrew JT;
XX
DR WPI; 2001-290726/30.
XX
PT An expression vector for increasing the yield of recombinant protein
PT comprises a first protein operably linked to a second protein.
XX
PS Claim 4; Page 28; 41pp; English.
XX
CC The present sequence is that of the SV40 late polyadenylation site. This
CC SV40 late polyadenylation site, or nucleotides 80-222 of it, is utilised

CC in a claimed expression vector. The vector comprises a promoter sequence, a first coding sequence, a polyadenylation site (preferably SV40 late or early polyadenylation site), and a second coding sequence, preferably encoding a selectable marker such as dihydrofolate reductase. The internal polyadenylation site allows a single promoter to generate both monocistronic messages and dicistronic messages. An internal ribosome entry site (IRES) may be inserted between the internal polyadenylation site and the DNA encoding the selectable marker. Similar, multicistronic vectors can also be prepared. Cells transfected with the vector, and cell lines cloned from them, are also claimed. These are used for obtaining a recombinant protein in mammalian host cells. The expression vector is useful as it comprises a selectable, amplifiable marker, while increasing the proportion of mRNAs encoding a desired recombinant protein

XX

SQ Sequence 222 BP; 76 A; 30 C; 45 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 222; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120

Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180

Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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RESULT 2
AAF30816/c
ID AAF30816 standard; DNA; 222 BP.
XX
AC AAF30816;
XX
DT 21-JUN-2001 (first entry)
XX
DE SV40 early polyadenylation site.
XX
KW SV40; polyadenylation; vector; ss.
XX
OS Rhesus macaque polyoma virus.
XX
PN WO200127299-A1.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028431.
XX
PR 13-OCT-1999; 99US-0159177P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Mcgrew JT;
XX
DR WPI; 2001-290726/30.
XX
PT An expression vector for increasing the yield of recombinant protein
PT comprises a first protein operably linked to a second protein.
XX
PS Claim 4; Page 28-29; 41pp; English.
XX
CC The present sequence is that of the SV40 early polyadenylation site. This
CC SV40 early polyadenylation site can be utilised in a claimed expression
CC vector. The vector comprises a promoter sequence, a first coding
CC sequence, a polyadenylation site (preferably SV40 late or early
CC polyadenylation site), and a second coding sequence, preferably encoding
CC a selectable marker such as dihydrofolate reductase. The internal
CC polyadenylation site allows a single promoter to generate both
CC monocistronic messages and dicistronic messages. An internal ribosome
CC entry site (IRES) may be inserted between the internal polyadenylation
CC site and the DNA encoding the selectable marker. Similar, multicistronic
CC vectors can also be prepared. Cells transfected with the vector, and cell
CC lines cloned from them, are also claimed. These are used for obtaining a
CC recombinant protein in mammalian host cells. The expression vector is
CC useful as it comprises a selectable, amplifiable marker, while increasing
CC the proportion of mRNAs encoding a desired recombinant protein
XX
SQ Sequence 222 BP; 71 A; 45 C; 30 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 222; DB 5; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 163

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 103

Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 43

Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db         42 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1
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RESULT 3
ADA50602
ID ADA50602 standard; DNA; 250 BP.
XX
AC ADA50602;
XX
DT 20-NOV-2003 (first entry)
XX
DE SV40 polyadenylation signal (late and early), SEQ ID NO:57.
XX
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
KW humoral response; cellular response; immune response; immunotherapy;
KW cancer; cytostatic; vaccine; gene therapy; SV40; ds.
XX
OS Simian virus 40.
XX
PN WO2003031569-A2.
XX
PD 17-APR-2003.
XX
PF 18-SEP-2002; 2002WO-US029640.
XX
PR 10-OCT-2001; 2001US-0328371P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;
PI Branigan PJ;
XX
DR WPI; 2003-393437/37.
XX
PT New nucleic acid vaccine, useful for eliciting an immune response to a
PT cancer associated tumor protein in a mammal.
XX
PS Disclosure; Page 50; 92pp; English.
XX
CC The invention relates to a nucleic acid vaccine comprising one or more

CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,
CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
CC is preferably under the control of a promoter such as the cytomegalovirus
CC immediate early promoter, the dihydrofoliate reductase promoter or the
CC early or late SV40 promoters. The invention also encompasses the method
CC of eliciting an immune response to a tumour antigen in a mammal using the
CC vaccine of the invention. Coexpression of the antigen and adjuvant
CC induces a humoral or cellular response to the tumour antigen, generating
CC an immune reponse useful for treatment or prophylaxis of cancers. The
CC present sequence represents a regulatory nucleic acid used in DNA vaccine
CC vectors of the invention.
XX
SQ Sequence 250 BP; 85 A; 33 C; 54 G; 78 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 8; Length 250;
Best Local Similarity 99.1%; Pred. No. 2.6e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 64

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 124

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        125 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 184

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        185 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 228
```

RESULT 4
AAD04943
ID AAD04943 standard; DNA; 667 BP.
XX
AC AAD04943;
XX
DT 17-JUL-2001 (first entry)
XX
DE Insert sequence in pRK80c plasmid.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; pRK80c plasmid; ds.
XX
OS Unidentified.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Example 2; Page 65; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific
CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene
CC trapping construct is useful for mutationally inactivating all cellular
CC genes. The present sequence is an insert sequence in plasmid pRK80c. The
CC insert sequence is the Cre or C31-Int mediated inversion product. The
CC pRK80b is used for sequencing the Cre or C31-Int mediated inversion
CC product
XX
SQ Sequence 667 BP; 180 A; 156 C; 157 G; 173 T; 0 U; 1 Other;

Query Match 94.6%; Score 210; DB 5; Length 667;
Best Local Similarity 99.1%; Pred. No. 3.2e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 388

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 448

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        449 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 508

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        509 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 552
```

RESULT 5
AAT97157
ID AAT97157 standard; DNA; 677 BP.
XX
AC AAT97157;
XX
DT 11-MAY-1998 (first entry)
XX
DE SV40 poly A signal.
XX
KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
KW gene amplification; immunotherapy; therapy; SV40; poly A signal; ds.
XX
OS Rhesus macaque polyoma virus.
XX
PN WO9741244-A1.
XX
PD 06-NOV-1997.
XX
PF 25-APR-1997; 97WO-US007039.
XX
PR 01-MAY-1996; 96US-00644664.
PR 06-DEC-1996; 96US-00761277.
XX
PA (GENI-) GENITOPE CORP.
XX
PI Denney DW;

XX
DR WPI; 1997-549743/50.
XX
PT Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at
PT least 2 different recombinant variable regions of immunoglobulin
PT molecules derived from B cell lymphoma cells.
XX
PS Disclosure; Page 103; 177pp; English.
XX
CC This genomic DNA fragment comprises the SV40 poly A signal. It is used as
CC a regulatory element in expression vectors designed for efficient
CC expression of genes in eukaryotic cells. The invention provides vectors
CC and improved methods for the expression and co-amplification of genes
CC encoding recombinant proteins in cultured cells. The methods permit the
CC isolation of cell lines which have co-amplified input recombinant
CC sequences which encode an amplifiable marker, one or more expression
CC vectors encoding a protein of interest and optionally a selectable
CC marker. The amplified cells provide large quantities of recombinant
CC proteins suitable for immunotherapy for treatment of lymphomas and
CC leukaemias. The methods permit the production of custom vaccines,
CC including multivalent vaccines that reflect the degree of somatic
CC variation found in a patient's tumour
XX
SQ Sequence 677 BP; 202 A; 144 C; 112 G; 219 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 2; Length 677;
Best Local Similarity 99.1%; Pred. No. 3.2e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 62

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 122

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 182

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        183 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 226
```

RESULT 6
AAA74636/c
ID AAA74636 standard; DNA; 717 BP.
XX
AC AAA74636;
XX
DT 05-DEC-2000 (first entry)
XX
DE Plasmid pNSE-p25 3' UTR and SV40 polyadenylation sequence.
XX
KW p25; cdk5 activator; SV40 polyadenylation signal; untranslated region;
KW UTR; neuron specific enolase; NSE; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; amyelolateral sclerosis;
KW Huntington's disease; traumatic brain injury; stroke; transgenic animal;
KW spinocerebellar degeneration; tau hyperphosphorylation; ds.
XX
OS Rous sarcoma virus.
XX
PN EP1026251-A2.
XX
PD 09-AUG-2000.
XX
PF 02-FEB-2000; 2000EP-00300797.
XX
PR 03-FEB-1999; 99US-0118478P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Ahlijanian MK, Mcneish JD;
XX
DR WPI; 2000-507252/46.
XX
PT New recombinant DNA molecule comprising gene encoding p25, useful for
PT producing transgenic animal to serve as model for Alzheimer's-associated
PT neurofibrillary tangle formation.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The present sequence is the 3' untranslated region (UTR) and SV40
CC polyadenylation signal sequence of plasmid NSE-p25. The plasmid also
CC contains the human cDNA for p25, an activator of the protein kinase cdk5,
CC operably linked to the rat neuron specific enolase (NSE) promoter. The
CC NSE-p25 transgene was used in the production of transgenic mice
CC overexpressing human p25. Overexpression of p25 is sufficient to produce
CC hyperphosphorylation of tau, which is seen in the neurofibrillary tangles
CC associated with Alzheimer's disease. The transgenic animals are useful as
CC in vivo systems for screening potential therapeutic compounds for their
CC ability to inhibit or prevent the production of hyperphosphorylated tau
CC and associated neuronal death. The transgenic animals are suitable for
CC use as disease models of neurodegenerative diseases and tau-related
CC pathologies, such as Alzheimer's disease, Parkinson's disease,
CC amyelolateral sclerosis, Huntington's disease, stroke, traumatic brain
CC injury, spinocerebellar degeneration. They are also useful as models of
CC cdk5/p25 and tau biochemistry, and to establish the role of the human p25
CC in the formation of hyperphosphorylated tau in neurodegenerative
CC conditions
XX
SQ Sequence 717 BP; 229 A; 129 C; 131 G; 228 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 3; Length 717;
Best Local Similarity 99.1%; Pred. No. 3.2e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 656

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 596

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        595 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 536

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        535 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 492
```

RESULT 7
AAD04942
ID AAD04942 standard; DNA; 770 BP.
XX
AC AAD04942;
XX
DT 17-JUL-2001 (first entry)
XX
DE Insert sequence in pRK80b plasmid.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; pRK80b plasmid; ds.
XX
OS Unidentified.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX

PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Example 2; Page 65; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific
CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene
CC trapping construct is useful for mutationally inactivating all cellular
CC genes. The present sequence is an insert sequence in plasmid pRK80b. The
CC insert sequence is the Cre or C31-Int mediated inversion product. The
CC pRK80b is used for sequencing the Cre or C31-Int mediated inversion
CC product
XX
SQ Sequence 770 BP; 208 A; 199 C; 174 G; 188 T; 0 U; 1 Other;

Query Match 94.6%; Score 210; DB 5; Length 770;
Best Local Similarity 99.1%; Pred. No. 3.3e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 494

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 554

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        555 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 614

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        615 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 658
```

RESULT 8
AAH20736/c
ID AAH20736 standard; DNA; 782 BP.
XX
AC AAH20736;
XX
DT 13-AUG-2001 (first entry)
XX
DE SV40 DNA fragment.
XX
KW Gene therapy; amniocyte; cytostatic; Ad5; E1A region; E1B region;
KW modified tropism; tumor; ss.
XX
OS Rhesus macaque polyoma virus.
XX
PN WO200136615-A2.
XX
PD 25-MAY-2001.
XX
PF 07-NOV-2000; 2000WO-EP010992.
XX
PR 18-NOV-1999; 99DE-01055558.
XX
PA (KOCH/) KOCHANEK S.
XX
PI Kochanek S, Schiedner G;
XX
DR WPI; 2001-343817/36.
XX
PT New permanent amniocyte cell lines, useful for producing viral gene
PT therapy vectors or mutant adenoviruses, express the adenoviral E1A and
PT E1B gene products.
XX
PS Example 1; Page 64; 72pp; German.
XX
CC This invention describes novel permanent amniocyte cell lines (A),
CC containing at least one nucleic acid (I) that causes expression of the
CC gene products (II) of the adenoviral E1A and E1B regions. (A) are used to
CC produce gene therapy vectors, especially adeno, adeno-associated, retro
CC or lenti viral vectors, particularly first- or second generation, large-
CC capacity or deleted adenoviral vectors. (A) are also used to produce
CC adenoviral mutants, optionally with modified tropism. The vectors may
CC express a wide range of therapeutic proteins or antisense RNAs.
CC Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
CC for treating tumors, they replicate in the cells but not significantly in
CC normal primary cells. (A) can be made efficiently, simply and
CC reproducibly. The products of the invention have cytostatic activity.
CC This sequence represents a DNA fragment derived from SV40 which is
CC described in the method of the invention
XX
SQ Sequence 782 BP; 250 A; 137 C; 134 G; 261 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 5; Length 782;
Best Local Similarity 99.1%; Pred. No. 3.3e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 716

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 656

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        655 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 596

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        595 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 552
```

RESULT 9
ADV21047/c
ID ADV21047 standard; DNA; 816 BP.
XX
AC ADV21047;
XX
DT 24-FEB-2005 (first entry)
XX
DE 4x-Polyadenylation element DNA.
XX
KW Genetic engineering; gene targeting; gene trapping;
KW internal ribosomal entry site; IRES; IGS; inducible gene silencer; ds.
XX

OS Unidentified.
XX
PN US2004241851-A1.
XX
PD 02-DEC-2004.
XX
PF 30-MAY-2003; 2003US-00448395.
XX
PR 30-MAY-2003; 2003US-00448395.
XX
PA (AMHP) WYETH.
XX
PI Askew GR, Kanki KL;
XX
DR WPI; 2005-011640/01.
XX
PT New inducible gene silencer, useful for conditionally knocking out and
PT altering gene function and genetic sequences, and for gene trapping and
PT targeting.
XX
PS Claim 8; SEQ ID NO 7; 41pp; English.
XX
CC The present invention relates to an inducible gene silencer comprising a
CC splice acceptor sequence, an internal ribosomal entry site (IRES)
CC sequence, a nucleotide sequence coding for a reporter protein, a
CC polyadenylation sequence and a pair of oppositely oriented recombination
CC site sequences, which cause single cycle inversions in the presence of a
CC suitable recombinase enzyme, flanking the elements cited above. The
CC invention is useful for conditionally knocking out and altering gene
CC function and genetic sequences and for gene trapping and targeting. The
CC present sequence is a 4x-Polyadenylation (4x-PolyA) element DNA. This
CC element DNA is used to construct the inducible gene siliencer (IGS).
XX
SQ Sequence 816 BP; 257 A; 169 C; 122 G; 268 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 14; Length 816;
Best Local Similarity 99.1%; Pred. No. 3.3e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 505

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 445

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        444 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 385

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        384 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 341
```

RESULT 10
ADY66741/c
ID ADY66741 standard; DNA; 816 BP.
XX
AC ADY66741;
XX
DT 19-MAY-2005 (first entry)
XX
DE 4X-polyadenylation sequence (4X-PolyA) SEQ ID NO:7.
XX
KW knockout gene trapping; gene targeting; inducible gene silencer; ds.
XX
OS Synthetic.
XX
PN CA2428972-A1.
XX
PD 30-NOV-2004.
XX
PF 30-MAY-2003; 2003CA-02428972.
XX
PR 30-MAY-2003; 2003CA-02428972.
XX
PA (AMHP) WYETH.
XX
PI Barton M, Askew GR, Kanki KL;
XX
DR WPI; 2005-049264/06.
XX
PT Conditional knockout gene targeting, involves transfecting vector
PT comprising gene silencer into host cell, delivering suitable recombinase
PT enzyme to host cell, to cause inducible gene silencer to invert into
PT active orientation.
XX
PS Claim 8; SEQ ID NO 7; 60pp; English.
XX
CC The invention relates to a method for conditional knockout gene trapping
CC or gene targeting. The method comprises: (a) preparing an inducible gene
CC silencer comprising a splice acceptor sequence, an internal ribosomal
CC entry site (IRES) sequence, a nucleotide sequence coding for a reporter
CC protein, a polyadenylation sequence, and a pair of oppositely oriented
CC recombination site sequences which cause single cycle inversions in the
CC presence of a suitable recombinase enzyme; (b) flanking the previously
CC identified elements; (c) inserting the inducible gene silencer into a
CC vector in an inert orientation; (d) transfecting the vector comprising
CC the inducible gene silencer into a host cell; and (e) delivering a
CC suitable recombinase enzyme to the host cell or to any organism deriving
CC from the host cell, at any desired time, to cause the inducible gene
CC silencer to invert into an active orientation, so that the inducible gene
CC silencer knocks out the functioning of a gene into which it has inserted
CC and expresses the reporter protein. The present sequence represents a 4X-
CC polyadenylation sequence (4X-PolyA) which can be used in an inducible
CC gene silencer from the present invention.
XX
SQ Sequence 816 BP; 257 A; 169 C; 122 G; 268 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 14; Length 816;
Best Local Similarity 99.1%; Pred. No. 3.3e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 505

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 445

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        444 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 385

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        384 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 341
```

RESULT 11
AAL42929
ID AAL42929 standard; DNA; 1193 BP.
XX
AC AAL42929;
XX
DT 06-AUG-2002 (first entry)
XX
DE Medaka ovarian cytochrome P450 aromatase gene and promoter sequence.
XX
KW Medaka; Japanese rice fish; gene; ds; phenotypic sex modification;
KW ovarian cytochrome P450 aromatase promoter; blocker molecule;
KW ovarian P450 aromatase; sexual development; single sex line production;
KW pest eradication.

XX
OS Oryzias latipes.
XX
PN WO200230183-A1.
XX
PD 18-APR-2002.
XX
PF 09-OCT-2001; 2001WO-AU001264.
XX
PR 09-OCT-2000; 2000AU-00000646.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Thresher R, Hinds L, Grewe P, Patil J;
XX
DR WPI; 2002-416816/44.
XX
PT Novel construct for modifying phenotypic sex in animals to distort
PT operational sex ratio of exotic pests, comprises a promoter activated
PT during sex-determining stage and blocker that alters normal sexual
PT development.
XX
PS Claim 9; Page 97-98; 121pp; English.
XX
CC The invention comprises a construct for modifying phenotypic sex in
CC animals. The construct contains a promoter (i.e. a medaka ovarian
CC cytochrome P450 aromatase promoter). The promoter is operably linked to a
CC second nucleic acid encoding a blocker molecule (i.e. medaka or zebrafish
CC ovarian P450 aromatase) that alters normal sexual development in the
CC animal. The construct is useful for altering phenotypic sex in animals
CC (e.g. fish). The construct is also useful in animal husbandry in
CC producing single sex lines and can therefore be used to distort the
CC operational sex ratio - leading to reproductive failure, population
CC decline and eradication of a pest population. The construct can also be
CC used to alter sexual development in animals which induces sterility or
CC modifies phenotypic sex. The present DNA sequence represents the medaka
CC ovarian cytochrome P450 aromatase gene and promoter sequence
XX
SQ Sequence 1193 BP; 341 A; 260 C; 276 G; 316 T; 0 U; 0 Other;

Query Match 94.6%; Score 210; DB 6; Length 1193;
Best Local Similarity 99.1%; Pred. No. 3.5e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 962

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 1022

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1023 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 1082

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db       1083 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1126
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RESULT 12
AAL02861
ID AAL02861 standard; DNA; 1223 BP.
XX
AC AAL02861;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5549.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001339.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 13-OCT-2000; 2000US-0239937P.
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PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249245P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 06-DEC-2000; 2000US-0251479P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 5549; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 1223 BP; 363 A; 255 C; 264 G; 340 T; 0 U; 1 Other;

Query Match 94.6%; Score 210; DB 4; Length 1223;
Best Local Similarity 99.1%; Pred. No. 3.5e-43;
Matches 222; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 61

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 121

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        122 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 181

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||||
Db        182 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 225
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RESULT 13
AAS41785
ID AAS41785 standard; DNA; 1359 BP.
XX
AC AAS41785;
XX
DT 17-DEC-2001 (first entry)
XX
DE Genomic sequence #101 encoding novel human enzyme polypeptide.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 08-NOV-2000; 2000US-0246474P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Disclosure; SEQ ID NO 1911; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the

```
CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC   DNA sequences encoding for the novel human enzyme polypeptides of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1359 BP; 395 A; 301 C; 303 G; 360 T; 0 U; 0 Other;

  Query Match             94.6%;  Score 210;  DB 4;  Length 1359;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-43;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 180

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 224


RESULT 14
AAS41797
ID   AAS41797 standard; DNA; 1359 BP.
XX
AC   AAS41797;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Genomic sequence #113 encoding novel human enzyme polypeptide.
XX
KW   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW   anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155301-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001239.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
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PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Disclosure; SEQ ID NO 1923; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC DNA sequences encoding for the novel human enzyme polypeptides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Qy 121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
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KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
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XX
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XX
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XX
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CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
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CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
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CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
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CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders

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CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAS41685-AAS42192 represent
CC   DNA sequences encoding for the novel human enzyme polypeptides of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
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c 40		210	94.6	3485	11	UCU89962	U89962 Cloning vec
41		210	94.6	3487	11	PSBC1	X68257 Bicistronic
42		210	94.6	3639	11	SYNPKA1	D13749 Unidentifie
43		210	94.6	3740	6	AR262814	AR262814 Sequence
44		210	94.6	3807	11	CVU51223	U51223 Cloning vec
c 45		210	94.6	3900	6	I07249	I07249 Sequence 9

ALIGNMENTS

RESULT 1
AR408763
LOCUS AR408763 222 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6632637.
ACCESSION AR408763
VERSION AR408763.1 GI:40159158
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 222)
AUTHORS McGrew,J.T.
TITLE Vectors and methods for recombinant protein expression
JOURNAL Patent: US 6632637-A 1 14-OCT-2003;
Immunex Corporation; Seattle, WA
FEATURES Location/Qualifiers
source 1. .222
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 222; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 8.2e-36;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Db         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120

Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180

Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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RESULT 2
AR408765/c
LOCUS       AR408765                222 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 3 from patent US 6632637.
ACCESSION   AR408765
VERSION     AR408765.1  GI:40159160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 222)
  AUTHORS   McGrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: US 6632637-A 3 14-OCT-2003;
            Immunex Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 222;  DB 6;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-36;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 163

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 103

Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
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Db        102 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 43

Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db         42 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1


RESULT 3
AX113060
LOCUS       AX113060                222 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 1 from Patent WO0127299.
ACCESSION   AX113060
VERSION     AX113060.1  GI:13939494
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Mcgrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: WO 0127299-A 1 19-APR-2001;
            Immunex CorporatioN (US)
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="Simian virus 40"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
ORIGIN

  Query Match             100.0%;  Score 222;  DB 6;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-36;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Db         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120

Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180

Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222


RESULT 4
AX113062/c
LOCUS       AX113062                222 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 3 from Patent WO0127299.
ACCESSION   AX113062
VERSION     AX113062.1  GI:13939496
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Mcgrew,J.T.
  TITLE     Vectors and methods for recombinant protein expression
  JOURNAL   Patent: WO 0127299-A 3 19-APR-2001;
            Immunex CorporatioN (US)
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="Simian virus 40"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
ORIGIN

  Query Match             100.0%;  Score 222;  DB 6;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-36;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db        222 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 163

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Db        162 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 103

Qy        121 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 180
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Db        102 GCAATAAACAAGTTCAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTG 43

Qy        181 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||
Db         42 TGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 1


RESULT 5
HSA332357
LOCUS       HSA332357               573 bp    DNA     linear   PRI 18-JUL-2002
DEFINITION  Homo sapiens genomic sequence surrounding NotI site, clone
            HSJ4P-P16RS.
ACCESSION   AJ332357
VERSION     AJ332357.1  GI:15876775
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
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            Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
  TITLE     NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
  JOURNAL   Nucleic Acids Res. 30 (14), 3163-3170 (2002)
   PUBMED   12136098
REFERENCE   2  (bases 1 to 573)
  AUTHORS   Zabarovsky,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="HSJ4P-P16RS"
ORIGIN

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  Best Local Similarity   99.1%;  Pred. No. 1.9e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

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Db         27 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 86

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 146

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
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Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db        207 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 250


RESULT 6
AX114869
LOCUS       AX114869                667 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 29 from Patent WO0129208.
ACCESSION   AX114869
VERSION     AX114869.1  GI:14031811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 29 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA sequence derived from vector pRK80c"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 667;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db        329 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 388

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        389 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 448

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
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Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db        509 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 552


RESULT 7
AR016495
LOCUS       AR016495                677 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5776746.
ACCESSION   AR016495
VERSION     AR016495.1  GI:3972772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Denney,D.W. Jr.
  TITLE     Gene amplification methods
  JOURNAL   Patent: US 5776746-A 3 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db          3 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 62

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 122

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 182

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db        183 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 226


RESULT 8
AR096878
LOCUS       AR096878                677 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 3 from patent US 5972334.
ACCESSION   AR096878
VERSION     AR096878.1  GI:10009402
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Denney,D.W. Jr.
  TITLE     Vaccines for treatment of lymphoma and leukemia
  JOURNAL   Patent: US 5972334-A 3 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .677
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 677;
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  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db          3 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 62

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 122

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
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Db        123 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 182

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db        183 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 226


RESULT 9
BD136073
LOCUS       BD136073                677 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vaccines for treatment of lymphoma and leukemia.
ACCESSION   BD136073
VERSION     BD136073.1  GI:23231018
KEYWORDS    JP 2002509426-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Jr,D.W.D.
  TITLE     Vaccines for treatment of lymphoma and leukemia
  JOURNAL   Patent: JP 2002509426-A 3 26-MAR-2002;
            GENITOPE CORP
COMMENT     OS   Unidentified
            PN   JP 2002509426-A/3
            PD   26-MAR-2002
            PF   25-APR-1997 JP 1997539097
            PR   01-MAY-1996 US    08/644664,06-DEC-1996 US    08/761277 PI
            DAN W DENNEY JR
            PC   C12N15/86,C12N15/63,C12N15/00,C12P19/24,A61K39/395,C07H21/04
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   Vaccines for treatment of lymphoma and leukemia FH   Key
             Location/Qualifiers
            FT   source          1. .677
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .677
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match            94.6%;  Score 210;  DB 6;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
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Db          3 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 62

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Db         63 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 122

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        123 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 182

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
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Db        183 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 226


RESULT 10
AR476069/c
LOCUS       AR476069                717 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 3 from patent US 6693226.
ACCESSION   AR476069
VERSION     AR476069.1  GI:42716014
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   McNeish,J.D. and Ahlijanian,M.K.
  TITLE     Transgenic mice expressing human p25
  JOURNAL   Patent: US 6693226-A 3 17-FEB-2004;
            Pfizer Inc; New York, NY
FEATURES              Location/Qualifiers
     source           1. .717
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match            94.6%;  Score 210;  DB 6;  Length 717;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 656

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
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Db        655 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 596

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        595 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 536

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        535 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 492


RESULT 11
BD002329/c
LOCUS       BD002329                717 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Transgenic non-human animal having transgene encoding p25
            polypeptide and  transgenic non-human mammalian cell.
ACCESSION   BD002329
VERSION     BD002329.1  GI:18630290
KEYWORDS    JP 2000224995-A/3.
SOURCE      Rous sarcoma virus
  ORGANISM  Rous sarcoma virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Alpharetrovirus.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Arijanian,M.K. and Macnesh,J.D.
  TITLE     Transgenic non-human animal having transgene encoding p25
            polypeptide and transgenic non-human mammalian cell
  JOURNAL   Patent: JP 2000224995-A 3 15-AUG-2000;
            PFIZER PROD INC
COMMENT     OS   Rous sarcoma virus
            PN   JP 2000224995-A/3
            PD   15-AUG-2000
            PF   03-FEB-2000 JP 2000026792
            PR   03-FEB-1999 US    60/118478
            PI   MICHAEL KIRK ARIJANIAN,JOHN DOUGLAS MACNESH
            PC   C12N15/09,A01K67/027,A61K45/00,A61P25/28,C12N5/10,C12N9/12, PC
              C12N9/99//
            PC   G01N33/15,G01N33/50,(C12N5/10,C12R1:91),C12N15/00,C12N5/00, PC
              (C12N5/00,C12R1:91)
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          CC
          FH   Key             Location/Qualifiers
          FT   source          1. .717
          FT                   /organism='Rous sarcoma virus'.
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="Rous sarcoma virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:11886"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 717;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-33;
  Matches  222;  Conservative .  0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 656

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 596

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        595 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 536

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        535 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 492


RESULT 12
AX114868
LOCUS       AX114868                770 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 28 from Patent WO0129208.
ACCESSION   AX114868
VERSION     AX114868.1  GI:14031810
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 28 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA squence derived from vector pRK80b"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 770;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 494

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 554

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        555 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 614

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        615 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 658


RESULT 13
AR310572/c
LOCUS       AR310572                782 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8 from patent US 6558948.
ACCESSION   AR310572
VERSION     AR310572.1  GI:31703586
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 782)
  AUTHORS   Kochanek,S. and Schiedner,G.
  TITLE     Permanent amniocytic cell line, its production and use for the
            production of gene transfer vectors
  JOURNAL   Patent: US 6558948-A 8 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 716

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 656

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        655 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 596

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        595 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 552


RESULT 14
AX150253/c
LOCUS       AX150253                782 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 8 from Patent WO0136615.
ACCESSION   AX150253
VERSION     AX150253.1  GI:14348273
KEYWORDS    .
SOURCE      Simian virus 40
  ORGANISM  Simian virus 40
            Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
REFERENCE   1
  AUTHORS   Kochanek,S. and Schiedner,G.
  TITLE     Permanent amniocyte cell line, the production thereof and its use
            for producing gene transfer vectors
  JOURNAL   Patent: WO 0136615-A 8 25-MAY-2001;
            Kochanek, Stefan (DE)
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="Simian virus 40"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10633"
                     /note="3'-Spleiss- und Polyadenylierungssignal von SV40
                     aus Plasmid pGL2basic, entsprechend bp 1978-2749, Genbank
                     X65323"
ORIGIN

  Query Match             94.6%;  Score 210;  DB 6;  Length 782;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-33;
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  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 716

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 656

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        655 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 596

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        595 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 552


RESULT 15
AY590429/c
LOCUS       AY590429               1096 bp    DNA     linear   SYN 05-AUG-2004
DEFINITION  Cloning vector pACCMVpLpARS(+), partial sequence.
ACCESSION   AY590429
VERSION     AY590429.1  GI:46370406
KEYWORDS    .
SOURCE      Cloning vector pACCMVpLpARS(+)
  ORGANISM  Cloning vector pACCMVpLpARS(+)
            other sequences; artificial sequences; vectors.
REFERENCE   1  (bases 1 to 1096)
  AUTHORS   Sapag,A., Munoz-Brauning,C. and Israel,Y.
  TITLE     Hammerhead ribozymes decrease the activity of rat mitochondrial
            aldehyde dehydrogenase (ALDH2)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1096)
  AUTHORS   Munoz-Brauning,C. and Sapag,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2004) Laboratorio de Farmacoterapia Genica,
            Departamento de Quimica Farmacologica y Toxicologica, Facultad de
            Ciencias Quimicas y Farmaceuticas, Universidad de Chile, Olivos
            1007, Independencia, Santiago 8380492, Chile
FEATURES             Location/Qualifiers
     source          1. .1096
                     /organism="Cloning vector pACCMVpLpARS(+)"
                     /mol_type="other DNA"
                     /db_xref="taxon:271169"
     promoter        1. .362
                     /note="CMV IE1; similar to GenBank Accession Number
                     X03922"
     TATA_signal     329. .333
     misc_feature    356
                     /note="transcription start site"
     misc_feature    372. .428
                     /note="multiple cloning site"
     misc_feature    431. .576
                     /note="portion of SV40 genome; similar to GenBank
                     Accession Number J02400"
     misc_feature    572. .866
                     /note="portion of SV40 genome; similar to GenBank
                     Accession Number J02400"
     polyA_signal    763. .768
                     /note="SV40"
     polyA_signal    792. .797
                     /note="SV40"
     misc_feature    881. .1096
                     /note="portion of adenovirus type 5 genome; similar to
                     GenBank Accession Number X02996"
ORIGIN

  Query Match           94.6%;  Score 210;  DB 11;  Length 1096;
  Best Local Similarity  99.1%;  Pred. No. 1.6e-33;
  Matches  222;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 ATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAA 806

Qy         61 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT 746

Qy        121 GCAATAAACAAGTT--CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 178
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        745 GCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGG 686

Qy        179 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 222
              |||||||||||||||||||||||||||||||||||||||||||
Db        685 TGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGT 642


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